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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   197
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213
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5 AY25516
5 AY2704249
5 AY204249
5 AY204245
5 AF345931
5 AY551929
5 AF367868
   AR287876
TGTRIGRA
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                                                                                              AY005480 Gloydius
AF051789 Gloydius
AY259516 Bothrops
AY204249 Gloydius
AY204245 Gloydius
AY204245 Gloydius
AF34931 Bothrops
AY551929 Gloydius
AF054626 Gloydius
D28870 Agkistrodon
E05552 cDNA encodi
AX009242 Sequence
AF367867 Gloydius
AF051788 Gloydius
AF051789 Gloydius
AF05877 Trimeresu
E39840 Anticancer
AR2876 Sequence
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AF212305 Agkistrod
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Matches 213; Conserv
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1 (bases 1 to 222)
Chung, K.-H., Koh, Y.-S., Hong, S.-Y. and Kim, D.-S.
Snake venom disintegrin, saxatilin cDNA
Unpublished
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Gloydius halys saxatilin
AY005480
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Chung, K.-H., Koh, Y.-S., Hong, S.-Y. and Kim, D.-S.
Direct Submission
                                                                                                                                                                                                                                                                                    Submitted (24-JUL-2000) Biochemistry, Yonsei Univ., Seodaemun Ku
Shinchon Dong 134, Seoul 120-749, Korea
Location/Qualifiers
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/protein_id="AAG01882.1"
/db_xref="GI:9945028"
/translation="EAGEECDCGAPANFCCDAATCKLRPGAQCAEGLCCDQCRFMKEG
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<1. .222
                                                                                                                                                                                                                       organism="Gloydius halys"
/mol_type="mRNA"
/db_xref="taxon:8714"
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100.0%; Score 213; DB 5;
100.0%; Pred. No. 4.3e-57;
tive 0; Mismatches 0;
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Gloydius halys
Gloydius halys
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepidosauria; Squamata; Scleroglossa; Serpentes; Viperidae; Crotalinae; Gloydius.

1 (bases 1 to 1989)

Jeon, O. H. and Kim, D. S.

Molecular cloning and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF051789 1989 bp mRNA Gloydius halys metalloprotease (Mt-d) mRNA, AF051789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-MAR-1998) Biochemistry, Yonsei University, Shinchon-Dong Seodaemun-Gu, Seoul 120-749, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1989)
Jeon, O.H. and Kim, D.S.
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GGAGTTGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA 1343
                   GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA 60
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                                                                       Conservative
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51. .1499
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                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/db_xref="GI:4106005"
                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Mt-d"
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/db_xref="taxon:8714"
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|mol_type="mRNA"
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Pred. No. 4.5e-56;
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1 (bases 1 to 234)

Ramos,O.H.P. and Selistre-de-Araujo,H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-MAR-2003) Depto. de Ciencias Fisiologicas,
Universidade Federal de Sao Carlos, Rodovia Washington Luis
(SP-310), Km 235, Sao Carlos, Sao Paulo 13565-905, Brazil
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY259516
Bothrops alternatus disintegrin
AY259516
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                                                                                   GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA
                                                                                                                                                                                                   GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
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                                                                                                                     CTGAGACCAGGGGGGGAGTGTGCAGAAGGACTGTGTGTGACCAGTGCAGATTTATGAAA
                                                                                                                                          CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA
                                                                                                                                                                                GGAGAAGAATGTGACTGTGGCACTCCTGGAAATCCGTGCTGCGATGCTGCAACCTGTAAA
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                                                           GAAGGAACAGTATGCCGGATTGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA
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                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="disintegrin"
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/db_xref="01:29501768"
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MKEGTVCRIARGDDMDDYCNGISAGCPRNPFHA"
                                                                                                                                                                                                                                                                                                                                                                                                              disintegrins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:64174"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bothrops alternatus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .234
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expression of disintegrins f
                                                                                                                                                                                                                                                        97.0%;
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                          Score 206.6; DB 5
Pred. No. 4.8e-55;
D; Mismatches 4
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                                                                                                                                                                                                                                                                        DB 5; Length
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AY204249
LOCUS
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VERSION
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Best Local Similarity
Matches 206; Conserv
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Sun,D.-J. and Yang,T.-S.
Direct Submission
Submitted (17-DEC-2002) Biochemistry Lab, Frotier Medical Science Submitted, Jilin University, No. 13 Xinmin Streeet, Changchun,
                                                                                                                                                                                                     precursor, mRNA, AY204245
                                                                                                                                                                                                                 AY204245 IP77 bp mRNA linear VRT 01. Gloydius ussuriensis metalloproteinase/disintegrin ussurin precursor, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-DEC-2002) Biochemistry Lab, I
Institute, Jilin University, No. 13 Xinmin
Jilin 130021, China
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(bases 1 to 712)
Sun,D.-J. and Yang,T.-S.
Direct Submission
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                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Lepidosauria; Squamata; Scleroglossa; Serpentes;
Viperidae, Croralinae; Gloydius.
1 (bases 1 to 1977)
                                                                                                                                     Gloydius ussuriensis
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protein_id="AAP20644.1"
/protein_id="AAP20644.1"
/db_xref="d1:31322311"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gloydius ussuriensis"
/mol_type="mRNA"
/db_xref="taxon:35671"
/tissue_type="snake venom gland"
/country="China: northeast area"
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                                                                                                                                                                                     GI:31322302
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n Streeet, Chango
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'note="isolated from venom"

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Query Match
Best Local Similarity
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Bothrops
AF345931
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                                                                                                                                                                                                                                                                           Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 2045)
Silva,C.A., Martins de Camargo,A.C. and de Toledo Serrano,S.M. Molecular cloning of a cDNA encoding bothrostatin, a precursor RGD containing disintegrin from Bothrops jararaca venom
                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops jararaca (jararaca)
Bothrops jararaca
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                 Submitted (05-FEB-2001) Bioquimica e Biofisica, Av. Vital Brasil 1500, Sao Paulo 05503-900, Brasi Location/Qualifiers
                                                                                                                                                                             Silva, C.A., Martins de Camargo, A.C. and de Toledo Serrano, S.M. Direct Submission
                                                                                                                                                                                                                                                      Unpublished
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DEDPKMCGVTETNWESYEDIKKASPLVVTTYQRYVELVVAAHRMVTKXNGNLIIIRT
WYYEIFNTINEIYQRMNIHVALVGLEIWSNGDKIIVQSSADVTLDLFGTWGEIDLLKR
KSHDNAQLLTPTDFDGPTIGLAYVGTMCDPKRSTGVVQDFSPLNLLVAAVTMAHEIGHN
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/protein id="AAP20640.1"
/db_xref="GI:31322303"
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/db_xref="taxon:35671"
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Pred. No. 1.6e-53;
0; Mismatches 7;
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rtheast area"
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                                                                                                                                                                                                                                                                                   , a precursor venom
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RESULT 7
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                                                                                                                                                                                                      Submitted (19-FEB-2004) Department of Biochemistry and Molecular Biology, Dalian Medical University, 465 Zhongshan Road, Dalian, Liaoning 116027, China
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
1 (bases 1 to 270)
Wang, J.H., Wu,Y., Ren,F. and Zhao,B.C.
Cloning and characterization of adinbitor: a novel disintegrii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY551929 270 bp mRNA linear VRT 24-Gloydius blomhoffi brevicaudus adinbitor mRNA, partial cds AY551929
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gloydius blomhoffi brevicaudus Gloydius blomhoffi brevicaudus
                                                                                                                                                                                                                                                            2 (bases 1 to 270)
Zhao, B.C., Wang, J.H., Ren, F. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY551929.1 GI:50365990
                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
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                                                                                                                                                                                                                                                                                                                                    snake venom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MIEVLLVTICLAAFPYQGSSIILESGNVNDYEVIYPRKVTALPK
GAVQPKYEDAMOYELKNVGEPVVLHLEKNKGLFSKDYSETHYSPDGRKITTNPPVEDH
CYYHGRIENDADSTASISACNGLKGHFKLQGETYLIEPLKLSDSEAHAVFKFENVEKE
DEAFKMCGVTQKMESYEBIKKASQSNLTPEHQRYIELFLVVDHGMFMKKNGNSDKIRR
RIHQMVNIMKEAYRYLYIDIALTGVEIMSNKDMINVQPAAPQTLDSFGEMRKTDLLNR
KSHDNAQLLTSTDFKDQTIGLAYWGSMCDPKRSTAVIEDHSETDLLVAVTMAHELGHN
LGIRHDTGSCSCGGYSCIMAPVISHDIAKYFSDCSYIQCMDFIMKDNPQCILNKQLRI
LGIRHDTGSCSCGGYSCIMAPVISHDIAKYFSDCSYIQCMDFIMKDNPQCILNKQLRI
TDTVSTPVSGKNFCAGEEDDCGTPGNPCCDAVTCKLRPGAQCAEGLCCDQCRFMKEGTV
CRRARGDDMDDYCNGISAGCPRNPFHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86. .1519
/note="RGD-containing disintegrin"
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/db_xref="GI:13194760"
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/protein_id="AAK15542.1"
/codon_start=1
/product="adinbitor"
                                                                     /tissue_type="venom gland"
<1. .270</pre>
                                                                                                     /organism="Gloydius blomhoffi brevicaudus"

'mal_type="mRNA"

'sub_species="brevicaudus"

'db_xref="taxon:259325"
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                                                                                                                                                                                         location/Qualifiers
                               function="inhibits platelet aggregation and angiogenesis"
note="contains a disintegrin-like domain"
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Pred. No. 1.6e-53;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                 Wu,Y.
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Query Match 93.
Best Local Similarity 95.
Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 bp mRNA linear VRT 0. Gloydius halys brevicaudus platelet aggregation inhibitor disintegrin (salmosin) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
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Gloydius blomhoffi brevicaudus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viperidae; Crotalinae; Gloydius.

1 (bases 1 to 318)

Kang, I.C., Chung, K.H., Lee, S.J., Yun, Y.D., Moon, H.M. and Kim, Rang, I.C., Chung and molecular cloning of a platelet aggregation inhibitor from the snake (Agkistrodon halys brevicaudus) venon Thromb. Res. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-MAR-1998) Biochemistry, Yonsei University, Science, 134 Seodaemoon-gu, Shinchon-Dong, Seoul 120-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/db xref="G1:50365991"
/tzanslation="MHREAGEECDCGSPGNPCCDAATCKLROGAQCAEGLCCDQCRFM
/txanslation="MHREAGEECDCGSPGNPFHAKLAAALEHHHHHH"
KKGTVCRIARGDDMDDYCNGISAGCPRNPFHAKLAAALEHHHHHHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 Seodaemoon-gu, |
Location/Qualifiers
                                                                                                                                   /product="platelet aggregation inhibitor disintegrin"
/protein id="AAC08997.1"
/brotein id="AAC08997.1"
/db xref="GI:3003025"
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/tranislation="WDFINNQKPQCILNKEGTICRRARGDDLDDYCNGISAGCPRNP
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:259325"
                                                                                                                                                                                                                                                                                                                                                                                                  'gene="salmosin"
                                                                                                                                                                                                                                                                                                                                                                                    sub_species="brevicaudus"
                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                    'gene="salmosin"
                       93.2%;
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Pred. No. 1.8e
0; Mismatches
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    Score 198.6; DB 5
Pred. No. 1.8e-52;
0; Mismatches 9
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1.8e-52;
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         Gaps
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AF367868.1
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Submitted (02-APR-2001) Biochemistry, Guar
Submitted (02-APR-2001) Guangxi 530021,
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Gloydius halys brevicaudus
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1 (bases 1 to 972)
                                                                                                                                                                                                      Similarity
GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA
                                                                      CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
                                                                                                                   GGAGAAGAATGTGACTGTGGCTCTCCTGGAAATCCCGTGCTGATGCTGCAACCTGTAAA
                                                                                                                                                   GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA 60
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                                                    CTGAGACAAGGAGCACAGTGTGCAGAAGGACTGTTGTGACCAGTGCAGATTTATGAAA
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                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="hxl-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="venom gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="disintegrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="hxl-1"
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Pred. No. 1.8e-52;
0; Mismatches 9
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                                                                                                               1 GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
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Submitted (08-MaR-1994) Shun-ichi Kuroda, Osaka University,
Submittede (06-MaR-1994) Shun-ichi Kuroda, Osaka University,
Institute of Scientific and Industrial Research, Department
Structural Molecular Biology; 8-1 Mihogaoka, Ibaraki, Osaka
567-0047, Japan (E-mail:skuroda@sanken.osaka-u.ac.jp,
Tel:81-6-6879-8462, Fax.81-6-6879-8464)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujisawa,Y., Kuroda,S., Notoya,K., Konishi,H. and Terashita,Z. Halystatin, a novel disintegrin from agkistrodon halys, is a pinhibitor of bone resorption and platelet aggregation J. Takeda Res. Lab. 53, 39-56 (1994)
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Gloydius halys
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                                          CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA
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                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="ucro-
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1183. .1449
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LLNRTSHDHAQLMTATIFNGNVIGRAPVGGMCDPXRSVAIVRDHNAILFIVAVTMTHE
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                                                                                                                                                                                                                                                                                      'product="disintegrin region"
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                                                                                                                                                                                              Score 198.6; DB 5;
Pred. No. 1.7e-52;
0; Mismatches 9;
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AUTHORS
Pujisawa, Y. and Kuroda, S.
Patent: JP 1993255395-A 1 05-OCT-1993;
TAKEDA CHEM IND LTD

COMMENT
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PN JP 1993255395-A/1
PD 05-OCT-1991 JP 1991256234
PR 26-OCT-1990 JP 90P 287116, 20-FEB-1991 JP 91P 26328 PI
FUJISAWA YUKIO, KURODA SHNUTCHI
PC COTKISJO4, COTKISJO9, C12N15/12, C12P21/02//A61K37/02;
CC strandedness: Double;
CC *source: tissue_Type=venom-secreting gland;
FH Key
FT 5/UTR
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           RESULT 12
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                                                                                        TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC 213
                                                                                                                                              GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
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location/Qualifiers
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222 bp
from Patent EP0967276.
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Pred. No. 1.7e-52;
0; Mismatches 9;
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AX009242.1
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917 bp mRNA linear Gloydius halys brevicaudus metalloproteinase-like partial sequence.
AF367867
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Gloydius blomhoffi brevicaudus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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Anti-tumor agent comprising salmosin
Patent: EP 0967276-A 3 29-DEC-1999;
                                                                                                                                                                                                        Submitted (02-APR-2001) Biochemistry, Guangxi Medical University, Shuangyong Road, Nanning, Guangxi 530021, China NCBI staff are still waiting for submitters to provide appropriate coding region information.
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                                                                                                                                                                                                                                                                                                            Xilian,H.
Direct Submission
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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                                         /organism="Gloydius blomhoffi brevicaudus"
/mol_type="mRNA"
/sub_species="brevicaudus"
/db_xref="taxon:259325"
<1. -.917
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|sub_species="brevicaudus"
|db_xref="taxon:259325"
/note="similar
                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 5.8e-52;
0; Mismatches 10
to metalloproteinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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KEYWORDS
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AF051788
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                                                                                   Query Match
Best Local Simi
Matches 203;
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Best Local Similarity
Matches 203; Conserv
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 61
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Gloydius halys
Gloydius halys
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.

1 (bases 1 to 2027)
Jeon,O.H. and Kim,D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (03-MAR-1998) Biochemistry, Yonsei University,
Shinchon-Dong Seodaemun-Gu, Seoul 120-749, Korea
Location/Qualifiers
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Gloydius halys metalloprotease
AF051788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF051788.1
                                                                                                    Similarity
                                               GGAGAAGAATGTGACTGTGGGGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
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CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
                            GGAGAAGAATGTGACTGTGGCTCTCCTGGAAATCCGTGCTGTGATGCTGCAACCTGTAAA 1380
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nilarity 95.3%;
Conservative
                                                                                      Conservative
                                                                                                                                                                      ATCKLRQGAQCAEGLCCDQCRFMKEGTICRRGRGDDLDDYCNGISAGCPRNPFHA"
                                                                                                                                                                                                                                                                                                                                                                    /gene="Mt-b"
19. .1536
                                                                                                                                                                                                                                                                                                                                                    'gene="Mt-b"
                                                                                                                                                                                                                                                                                                                                                                                                   /strain="brevicaudus"
/db_xref="taxon:8714"
/tissue_type="venom"
1. .2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Gloydius halys"
                                                                                                 92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="mRNA"
                                                                                    Score 197; DB 5; I
Pred. No. 5.7e-52;
O; Mismatches 10;
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Pred. No. 5.7e-52;
0; Mismatches 10;
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1303 GGAGAAGAATGTGACTGTGGCTCTCCTGAAAATCCGTGCTGCGATGCTGCAACCTGTAAA

1362

GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA

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Matches

202;

Conservative

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11;

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AUTHORS
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KEYWORDS
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ACCESSION
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AB059572
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                                                                  ORIGIN
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polyA_site
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Trimeresurus elegans
Trimeresurus elegans
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-APR-2001) Nobuhiro Murayama, Showa University, Schoof Pharmaceutical Sciences; 1-5-8 Hatanodai, Shinagawa-Ku, Tokyo 142-8555, Japan (E-mail:murayamagpharm.showa-u.ac.jp, Tel:81-3-3784-8203, Fax:81-3-3784-7550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1983)
Murayama, N. and Shimosaka, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trimeresurus elegans mRNA for elegantin-2a precursor,complete Published Only in Database (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB059572.1
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AB059572
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  Similarity
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/procdict="elegantin-2a precursor"
/procdict="elegantin-2a precursor"
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/translation="MICVILVTICLAVFPYQGSSITYLIEPLESDSEAHAVFKYENVEKE
GAVQRYSTEDAVQYEFXVNGEAVVLHLEKNKGLFSEDYSSTYLIEPLESDSEAHAVFKYENVEKE
CYYHGRIHNDADSTASISACDGLKGYFKLQGETYLIEPLELAIVVDHGMYTKYSSNFK
KIRKRVHQMYSNINJAMTALITLALLDVBSEDFITVQADAFTTAGLFGDMERAV
LLKKKNHDHAQLLTDTNFARNTIGMAYLIGRMCDEXYSVGVVQDHSSKVFMYAVTMTHE
LGHNLGMEHDDNECKCEACINSAVISDKQSKLFSDCSKYQTFLTNDNPQCILNAP
LRTDTVSTYSTPVGGNEFLEAGEECDCGSERNCCDAATCKLRPGAQCADGLCCDQCRFIE
LGGITCRARGDDLDDYCNGISGDCPRNPFHA"
                                                                                                                                /note="metalloproteinase-like 1962..1967
                                                                                                                                                                                                                          1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:88086"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                        'note="19 A nucleotides"
                                                                                                                                                                                                     /product="disintegrin elegantin-2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Trimeresurus elegans"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ssue_type="venom
.1518
91.7%;
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  Score 195.4; DB 5; Pred. No. 1.8e-51;
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r elegantin-2a precursor,
                                                                                                                                                          domain"
                     Length 1983;
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r, complete cds.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 EAGEECDCGAPANPCCDAAT....
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AC Q9
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Best Local S
Matches 73
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TISSUE-VERONG Gland;
Chung K.-H., Koh Y.-S., Hong S.-Y., K.
Submitted (JUL-2000) to the EMBL/GenB.
EMBL, AY005480; AAGOIR82.1; -.
InterPro; IPR001762; Disintegrin.
Pfam; PF00200; Disintegrin; 1.
PRINTS; PR00209; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISINTEGRIN_1; 1.
PROSITE; PS00427; DISINTEGRIN_1; 1.
PROSITE; PS00427; DISINTEGRIN_2; 1.
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SEQUENCE 73 AA; 7726 MM; 8F0225BBI
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01-NOV-1996 (TrEMBI
01-OCT-2003 (TrEMBI
Prepro-hallystatin 2
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01-MAR-2001
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Bukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.

NCBI TaxID=8714;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Saxatilin (Fragment).
Agkistrodon halys pallas (Chinese water mocassin)
                         Agkistrodon halys pallas).
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                                      (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
statin 2 (Fragment).
halys pallas (Chinese water mocassin) (
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  Chordata;
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the EMBL/GenBank/DDBJ
                                                  (Chinese water mocassin) (Gloydius halys
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DISI_BOTJA
DISI_CROMM
DISI_BOTCO
DISI_CROVL
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DIS2_AGKCA
DISI_SISBA
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Pred. No. 3.5
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     Euteleostomi;
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Query Match

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Best Local S
Matches 72
STRAIN-Brevication:

STRAIN-Brevication:

MEDLINE-99337693; PubMed=10406963;

Vacon O.H., Kim D.S.;

"Molecular cloning and functional characterization of a metalloprotease.";

Eur. J. Biochem. 263:526-533(1999).

Eur. J. Biochem. 263:526-533(1999).

EMEL; APS51789; AAD02654.1; -.

RMEL; APS51789; AAD02654.1; -.

RMEL; APS51789; Pimetalloendopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

RINEEPRO; IPR001762; Disintegrin.

RINEEPRO; IPR001590; Peptidase_M12B.

InterPro; IPR002590; Peptidase_M12B.

InterPro; IPR002590; Peptidase_M12B.

RINEEPRO; IPR006025; Pept_M 3r_BS.

Pfam; PF00200; Disintegrin; 1.

Pfam; PF00200; Disintegrin; 1.
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Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
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EMBL; D28871; BAA06027.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PVK9;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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PROSITE; PS00427; DISINTEGRIN_1; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
NCBI TaxID=8714;
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Name=Mt-d;
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Viperidae; Crotalinae; Gloydius.
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Pred. No. 1.1e-
1; Mismatches
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Matches 72
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Best Local (
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PRINTS; PR00289; DISINTEGRIN.
PrODom; D000064; Disintegrin; 1.
SMART; SM0050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 482 AA; 53409 MW; C6014BBE87BC8B
Q7SZD5;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003
01-JUN-2003
01-MAR-2004
Disintegrin
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Pfam; PF00200; Disintegrin; 1.
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Q801Z4;
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ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN_1; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
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Viperidae; Crotalinae; E
NCBI_TaxID=64174;
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                                                                 Q7SZD5
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llarity 98.6%;
Conservative
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94.5%;
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Pred. No. 9.1e-35;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                         Score 420; DB 2;
Pred. No. 7.5e-35;
2; Mismatches 2;
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RESULT
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Best Local S
Matches 67
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Q75ZD9;
Q75ZD9;
Q1-QCT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Metalloproteinase/disintegrin ussurin.
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleoston
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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NCBI_TaxID=35671;
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ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1;
PROSITE; PS50214; DISINTEGRIN_2;
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Sun D.-J., Yang T.-S.;
EMBL; AY20424; AAP20644.1; -.
GO; GO:0007229; P:integrin-mediated
InterPro; IPR001/62; Disintegrin.
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Disintegrin (Fragment).
Agkistrodon caliginosus (Korean
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nilarity 91.8%;
Conservative
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Pred. No. 7.2e-34;
Mismatches 2
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PR00200; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRINTS; PR00689; DISINTEGRIN; 1.
PRODOM; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1
PROSITE; PS50214; DISINTEGRIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q78CP2 PREMIEWANDERS (778CP2; Q78CP2; Q78CP2) (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) 05-JUL-2004 (TremBlrel 27, Last sequence update) 05-JUL-2004 (TremBlrel 27, Last annotation updat
                                        Q90WC0;
Q90WC0;
01-DEC-2001
01-DEC-2001
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kang I.C., Chung K.H., Lee S.J., Yun Y.D., Moon H.M., Kim D.S. "Purification and molecular cloning of a platelet aggregation inhibitor from the snake (Agkistrodon halys brevicaudus) venom Thromb. Res. 0:0-0(1998).

EMBL, AF054626, AAC08997.1; -.

GO, GO:0007229, P:integrin-mediated signaling pathway; IEA. InterPro; IPR001762; Disintegrin.

InterPro; IPR000519; P:trefoil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=259325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agkistrodon halys brevicaudus (Korean slamosa snake)
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                                                                                                                                                                                                                                                                                                                                                                                                                            68;
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                                                                                                                                                                                                                                                GISAGCPRNPFHA 105
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                                            (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
1 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
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                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
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                                            Last sequence update)
Last annotation update)
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Pred. No. 3.7e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            ₩.
                                                                                         Created)
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Pred. No. 1.2e-33;
2; Mismatches 3;
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.7e-33;
les 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 105
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Metalloproteinase Name=hxl-1;

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Best Local S
Matches 68
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GG; GG:0004222; F:metalloendopeptidase activity; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001599; Peptidase M12B.
InterPro; IPR001599; Peptidase M12B.
InterPro; IPR001599; Peptidase M12B.
PinterPro; IPR00159; Peptidase M12B.
InterPro; IPR00159; Peptidase M12B.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF00200; Disintegrin; 1.
PFINTS; PR00209; DISINTEGRIN.
ProDom; PR00209; DISINTEGRIN.
PRODOM; PR00209; DISINTEGRIN.
PRODOM; PR00209; DISINTEGRIN.
PRODOM; PR00209; DISINTEGRIN.
GO; GO:000422; F:metalloendopeptidase ac
GO; GO:0006508; P:proteolysis and peptido
InterPro; IPR001762; Disintegrin.
InterPro; IPR00150; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01563; Pep M12B propep; 1.
PRINTS; PR00289; DISINTEGRIN;
PRODOM; PR002664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
NON_TER 1 1
                                                                                                                                                   01-JUN-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xilian H.;
Submitted (APR-2001) to the
EMBL; AF367868; AAK73517.1;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                  Q98SP2;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Lepidosauria; Squamata; Sclerc
Viperidae; Crotalinae; Gloydiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agkistrodon halys brevicaudus brevicaudus)
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Bothrops jararaca (Jararaca).
                                                                                                                                                                                                                                                                                                                                                                               Q98SP2
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                                                                                                                                                                                                                                      NCBI_TaxID=8724;
                                                                                                                                                                                                                                                   Lepidosauria; Squamata;
Viperidae; Crotalinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAGEECDCGSPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317
                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35109 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.5%;
93.2%;
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; Scleroglossa; Serpentes; Colubroidea;
Gloydius.
                                                                                                                                                                                                                                                     Bothrops
                                                                                                                                                                                                                                                                                                                      17,
17,
26,
                                                                                                                                                                                                                                                                Scleroglossa;
                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 409; DB 2;
Pred. No. 3.2e-33;
2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; pglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Korean slamosa snake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9851177BCBE2202E
                                                                                                                         idase activity; IEA peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                               477
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                                                                                                                                                                                 databases.
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                                                                                                                                                                                              s.M.;
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RESULT
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 Query Match
Best Local S
Matches 67
                                                                                                                                                             MEROPS; M12.134; -...

GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Peptidase_M12B.
InterPro; IPR001590; Peptidase_M12B.
InterPro; IPR0002870; Peptidase_M12B.N.
InterPro; IPR0002870; Peptidase_M12B.N.
InterPro; IPR0002870; Pept_M.Zn_BS.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF001421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
PFAINTS; PR000289; DISINTEGRIN.
R PRINTS; PR000289; DISINTEGRIN.
R PRODOm; PD000664; Disintegrin; 1.
SMART; SM00055; DISINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                 Signal.
SIGNAL
CHAIN
CHAIN
SEQUENCE
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PROSITE; PSS0215; ADAM MEPRO; 1.

PROSITE; PSS00427; DISINTEGRIN 1; 1.

PROSITE; PSS0214; DISINTEGRIN 2; 1.

PROSITE; PS00142; ZINC PROTEASE; UNKNOWN SEQUENCE 477 AA; 53440 MW; AC973EE776
                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom gland;
Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashita
"Halystatin, a novel disintegrin from agkistrodon halys,
inhibitor of bone resorption and platelet aggregation.";
Takeda Kenkyusho Ho 53:39-56(1994).
EMBL; D28870; BAA06025.1; -.
EMBL; D28870; BAA06025.1; -.
PIR; A59410; A59411.
HRSP; P18619; IFVL.
                                                                                                               PROSITE; PS50215; ADAY MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS50214, DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prepro-halystatin precursor.
Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lepidosauria; Squamata; Scleroglossa;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pallas)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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 67; Conser
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67; Conserv
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190
392
480
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                   Ã,
                                                  18 P
391 P
480 P
53619 MW;
             94.5%;
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1; Mismatches
                                                                            Potential. Potential.
Score 409; DB 2; I
Pred. No. 4.6e-33;
4; Mismatches 2;
                                                  Potential.; 5CF5E6476511B3D7
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erpentes; Colubroidea;
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                                                     CRC64;
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                         Length
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  Indels
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EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN

60

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venom

peptide

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RESULT 12
DISI_AGKHA
ID DISI_A
AC P21858
DT 01-WAY
DT 01-WAY
DT 05-UUL
DE Disint
OS Agkist
OC Lepido
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073795
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:000422; F:metalloendopeptidase activity; IEA.
GO; GO:0004508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR00201; Peptidase M12B.
InterPro; IPR0020270; Peptidase M12B.
InterPro; IPR00201; Disintegrin; 1.
Pfam; PF001562; Pep M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOm; PD000664; Disintegrin; 1.
PRODOm; PD000664; Disintegrin; 1.
PROSITE; PS00164; Disintegrin; 1.
PROSITE; PS00125; ADAM MEPRO; 1.
PROSITE; PS00127; DISINTEGRIN 1; 1.
PROSITE; PS00127; DISINTEGRIN 1; 1.
PROSITE; PS00127; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
Metalloprotease; Protease.
                      DISI AGKHA STANDARD; PRT; 71 AA.

P21858;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Disintegrin halysin (Platelet aggregation activation inhibitor).
Agkistrodon halys blomhoffi (Mamushl) (Gloydius blomhoffii).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=brevicaudus; TISSUE=V
Jeon O.H., Kim D.S.;
Submitted (MAR-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palles).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Tarianana; Scieroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF051788; AAD02653.1;
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Viperidae; Crotalinae; Gloydius.
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                  GISAGCPRNPFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRWARGDDMDDYCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.5%;
nilarity 91.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56336 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 405; DB 2; I
Pred. No. 1.2e-32;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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    Serpentes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 505;
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                             Euteleostomi;
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                                                                                                                                                                                                                                                                                         DISI_AGKPI
ID DISI_AGKPI STANDARD;
ID DISI_AGKPI STANDARD;
ID DISI_AGKPI STANDARD;
ID DISI_AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-UUL-2004 (Rel. 44, Last annotation update).
DE Disintegrin applagin (Plattelet aggregation activation inhibitor).
DE Disintegrin applagin (Plattelet aggregation activation biscivorus piscivorus (Eastern cottonmouth).
OS Agkistrodon piscivorus piscivorus (Eastern cottonmouth).
OC Epidosauria, Squamata, Scleroglossa; Vertebrata; Euteleostomi;
OC Lepidosauria, Squamata, Scleroglossa; Scrpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
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DISI_AG
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Best Local S
Matches 65
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Interpro; IPRO01762; Disintegrin, 1
Pfam; PP00200; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS00427; DISINTEGRIN 2; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Halysin, an antiplatelet Arg-Gly-Asp-containing as fibrinogen receptor antagonist.";
Biochem. Pharmacol. 42:1209-1710***.
Chao B.H., Jakubowski J.A., Savage B., Ping Chow E., Marzec U.M., Harker L.A., Maraganore J.M.;
Harker L.A., Maraganore J.M.;
"Agkistrodon piscivorus platelet aggregation inhibitor: a potent inhibitor of platelet activation.";

Proc. Natl. Acad. Sci. U.S.A. 86.8050-8054(1989).

-I- FUNCTION: Inhibits fibrinogen interaction with platelet receptors expressed on glycoprotein IIb-IIIa complex. Acts by binding to the glycoprotein IIb-IIIa receptor on the platelet surface and inhibits aggregation induced by ADP, thrombin, platelet-activating factor and collagen.

-I- SUBCELLULAR LOCATION: Secreted.

-I- TISSUE SPECIFICITY: Expressed by the venom gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed on glycoprotein IIb-IIIa complex. Acts by binding to the glycoprotein IIb-IIIa complex. Acts by binding to the glycoprotein IIb-IIIa receptor on the platelet surface and inhibits aggregation induced by ADP, thrombin, platelet-activating factor and collagen.

SUBCELLULAR LOCATION: Secreted.

1 TISSUE SPECIFICITY: Expressed by the venom gland.
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NCBI_TaxID=242054;
[1]
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                                                                                                                                                                                                                                                                                 MEDLINE=90046735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sion; Direct protein sequencing;
By similarity.
Cell attachment site.
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2;
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2 CRC64;
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RESCRIPTION OF THE PROPERTY OF
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Best Local S
Matches 65
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SMART; SM00050; DISIN; 1.

PROSITE; PS00427; DISINTEGRIN 1; 1.

PROSITE; PS50214; DISINTEGRIN 2; 1.

Blood coagulation; Cell adhesion; D

Blood coagulation; Cell achesion; D

Blood coagulation; Cell achesion; Cell aches
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P63384; P17496;
O1-AUG-1990 (Rel. 15, Last sequence update)
O1-BUG-1990 (Rel. 15, Last annotation update)
O5-JUL-2004 (Rel. 44, Last annotation activation inhibitor).
Disintegrin albolabrin (Platelet aggregation activation inhibitor).
Trimeresurus albolabrin (White-lipped pit viper).
STRUCTURE BY NMR.
MEDLINE=97052455; PubMed=8897089;
Smith K.J., Jaseja M., Lu X., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calvete J.J., Schaefer \widetilde{W}., Soszká T., Lu W., Cook J.J., Jameson B., Niewłarowski S., "Identification of the disulfide bond pattern in albolabrin, an RG containing peptide from the venom of Trimeresurus albolabris: significance for the expression of platelet aggregation inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metażoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIAB
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PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=90283463; PubMed=2191722;
Williams J., Rucinski B., Holt J., Niewiarowski S.;
"Elegantin and albolabrin purified peptides from viper
homologies with the RGDS domain of fibrinogen and von W
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Hyde E.I.;
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                                                                                                                                         toxin, albolabri:
Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                            MEDLINE=94109384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91242430;
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                                                                                                                                                                                                   "1H-NMR studies and secondary structure
                                                                                                                                                                                                                                                                                                                                                    STRUCTURE
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                                                                                                                                                                                                                                                                                                                                                                                                                 liochemistry 30:5225-5229(1991).
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                                                                                                                                                                                                                                                                        К.J.,
                                                                                                                                     218:853-860(1993
                                                                                                                                                                                                                                                                        PubMed=8281937;
K.J., Lu X., Wil
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aefer W., Soszka
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Pred. No. 4e-32;
5; Mismatches 1;
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Cell attachment site.
B514FDE47D67E266 CRC64;
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   Williams J.A.,
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RESULT 15
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HSSP; P18619; 1FVL.
InterPro; IPR001762; Disintegrin.
Pfam; PF00200; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
PRODOM; P000069; DISIN; 1.
SNART; SM00050; DISIN; 1.
MEDLINE-90207217; PubMed=2320569;
Dennis M.S., Henzel W.J., Pitti R.M., Lipari M.T., Napier M.A.,
Deisher T.A., Bunting S., Lazarus R.A.;
"Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms:
evidence for a family of platelet-aggregation inhibitors.";
Proc. Natl. Acad. Sci. U.S.A. 87:2471-2475[1990].
-i- FUNCTION: Inhibits fibrinogen interaction with platelet receptors
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the
glycoprotein IIb-IIIa receptor on the platelet surface and
inhibits aggregation induced by ADP, thrombin, platelet-activating
factor and collagen.
-i- SUBCELLULAR LOCATION: Secreted.
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01-AUG-1990 (Rel. 15, Created)
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Disintegrin trigramin gamma (Platelet
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata;
Lepidosauria; Squamata; Scleroglossa; S
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. J. Pept. Protein Res. 48:220-228(1996).

-I- FUNCTION: Inhibits fibrinogen interaction with platelet receptors expressed on glycoprotein IIb-IIIa complex. Acts by binding to the glycoprotein IIb-IIIa receptor on the platelet surface and inhibits aggregation induced by ADP, thrombin, platelet-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Three-dimensional structure of the RGD-containing snake toxin albolabrin in solution, based on 1H NMR spectroscopy and simulated annealing calculations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
Blood_coagulation; Cell adhesion; D
                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                   NCBI_TaxID=8767;
                                                                                                                                                                                                                                                                          Trimeresurus gramineus (Indian
                                                                                                                                                                                                                                                                                           inhibitor).
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-1- TISSUE SPECIFICITY: Expressed by the venom gland.
-1- SIMILARITY: Belongs to the disintegrin family.
                                                                                                                                                                                                                                                                                                                                                                             TRIGA
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                                                                                                                                                                                                                                                                green tree viper) (Green habu snake).
Craniata; Vertebrata; Euteleostomi;
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aggregation
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16	w		73	œ	97	Adm10975 Ultrasoun
17	Ø	0	96	N	AAR28703	Aar28703 Bifunctio
18	w	0	96	N	870	28707
19	S	90.1	97	N	AAR28704	Aar28704 Bifunctio
20	v		97	N	AAR28706	8706
21	ø	0	99	N	515	r25153
22	9	0	99	N	514	r25149
23	Ø		$\sim$	N	AAR25148	25148
24	9		106	N	515	r25152
25	8	89.4	97	N	AAR28705	87

The invention relates to a cDNA encoding Saxatilin protein derived from venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is useful for as an anti-tumour agent and for effectively suppressing platelet aggregation which makes it possible as and an active ingredient of anti-platelet agent. Saxatilin is useful for inhibiting angiogenesis induced

New cDNA encoding Saxatilin protein derived from venom of Korean snake Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation agent and anti-tumor agent.

Claim 2; Page 35; 41pp; English.

WPI; 2002-241903/29. N-PSDB; AAD31060.

Hong S, Koh Y,

Sohn Ķ

You W,

Jang Y,

Huh C;

(CHUN/) CHUNG K. (KIMD/) KIM D.

26-JUL-2000; 2000WO-KR000809.

4 10	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30		28	27	4
356	356	356	360	368	368	371	371.5	372.5	375	379	379	382	384	384	384	386.5	387	387	387
•		82.2	٠	٠			85.8			•		•	88.7	œ	œ	9	89.4	9	89.4
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AAW50453	AAW46218	AAW46215	ABG70857	AAE03036	AAY79413	ADF65998	AAR53937	ADF66000	AAR10109	ADF65996	AAR10110	AAP91320	AAR25147	AAR25382	AAR25151	AAR53942	AAR25150	AAR25154	AAKZ81U8
٨a	Аa	Аа	æ	Aa	Aa	Ac	Ãа		Åa	Ac	Ac	Ae	Ac	. Аг	Ae	Аe	Aa	Αa	Ad
Aaw50453	Aaw46218	Aaw46215	Abg70857	Aae03036	Aay79413	Adf65998	Aar53937	Adf66000	Aar10109	Adf65996	Aar10110	Aap91320	Aar25147	Aar25382	Aar25151	Aar53942	Aar25150	Aar25154	Hd170/00
Snake ven	Snake ven	Snake ven	Disintegr	Agkistrod	Southern	Snake ven	Disintegr	Snake ven	Trigramin	Snake ven	Trigramin	New trigr	Bifunctio	Bifunctio	Bifunctio	Disintegr	Bifunctio	Bifunctio	BILUMCCIO

## ALIGNMENTS

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RESULT 1
AAB19787
ID AAB19787
ID 29-A
DT 07-A
DT 18-J
DT 20-L
XXX W0150
FT Misc
XXX W02(
XXX W01)
DR N-P
XXX WPI

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07-AUG-2003
18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korean snake; saxatilin; anticoagulant; cytostatic; venom; anti-tumour; platelet aggregation; angiogenesis; cytotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2000; 2000WO-KR000809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloydius halys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agkistrodon saxatilis emelianov saxatilin protein.
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(revised)
(first entry)
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1. .3
/note= "Encoded by GGA"
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                                              Query Match
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Matches 68
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by tumour and for inhibiting tumour without cytotoxicity. The present sequence is Agkistrodon saxatilis emelianov saxatilin protein. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise OS field)
                                                                                              Sequence 73
                                                                                                                                This peptide, designated Salmosin, inhibits blood platelet aggregation. It is derived from the venom of the Korean salmosa viper (Agkistrodon halys brevicaudus). Salmosin can be used, in particular, in compositions for management of thrombosis. Salmosin also has higher activity than kistrin, gamma-trigramin and echistatin. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                          Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gloydius halys
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27-OCT-1997
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                                                                                                                      kistrin, gamma-trigramin
standardise OS field)
                                                                                                                                                                                                                               Peptide derived from Korean salmosa viper venom - useful as blood platelet aggregation inhibitor, for the management of thrombosis.
                                                                                                                                                                                                                                                                     WPI; 1997-121376/12.
                                                                                                                                                                                                                                                                                                                                                        05-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Platelet aggregation inhibitor, Salmosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW14083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW14083 standard;
                                                                                                                                                                                                        Claim 1; Page 11; 15pp;
                                                                                                                                                                                                                                                                                                        In CK,
                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1997
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                                                 68
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                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viper;
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             EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GISAGCPRNPFHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 60
 EAGEECDCGS PGNPCCDAATCKLRQGAQCAEGLCCDQCR FMKEGT I CRRARGDDLDDYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibit; blood; platelet aggregation; venom; Korean;
iper; Agkistrodon halys brevicaudus; treatment; throm
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(first entry)
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                                                         94.5%;
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                                                                                                                                                                                                           French.
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                                                                                                                                                                                                                                                                                                       Doo SK, Hak DK,
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                                             Score 409; DB 2; I
Pred. No. 1.3e-29;
2; Mismatches 3;
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Pred. No. 9.2e-32;
Mismatches 0;
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60
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Matches Query Match

68;

Conservative

2

Score 409; DB 3; I Pred. No. 1.3e-29; 2; Mismatches 3;

Length 73; Indels

0

Gaps

60 60 0

EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN EAGEECDCGSPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDVCN

Similarity

94.5%;

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RESULT 3
AAXS 8231
ID AAXY
XX AAYS
XX AAYS
XX AAYS
XX AAYS
XX AAYS
DT 17-8
DT 17-8
DT 17-8
XX Core
XX 
                                              This sequence represents a 7.5 kD salmosin protein of a Korean snake, CC Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of CC small proteins mainly derived from snake venom which contain an RGD or CC XGD motif (the structural motif recognised by platelet fibringen CC receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of CC several integrins including alpha-y-beta-3 and alpha-5-beta-1 integrins, CC the former being a marker of angiogenic blood vessels and certain CC malignant cells. Disintegrins inhibit tumour metastasis by blocking CC tumour cell adhesion to the extracellular matrix, and antagonism of CC integrin alpha-y-beta-3 can suppress tumour-induced angiogenesis.
CC Salmosin can be used as an anticancer agent. It may be used for the CC inhibition or reduction of tumour cell angiogenesis, the inhibition of metastatic tumour formation and the inhibition or reduction of metastatic cumour growth. Nucleotides encoding salmosin may be used in gene therapy CC applications. Many types of cancer may be treated with salmosin or CC nucleotides encoding it, including leukaemia and cancers of the breast, CC ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain, CC muscle and bone. (Updated on 12-SEP-2003 to standardise OS field)
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      Sequence 73 AA;
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N-PSDB; AAZ55609.
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04-JUN-1999;
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27-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides used for antitumor therapy
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99KR-00020579.
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GISAGCPRNPFHA

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AC AAR4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                               New cDNA encoding Saxatilin protein derived from venom of Korean snake Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation agent and anti-tumor agent.
            AAR42867;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 38-39; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002
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18-JUN-2002
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                                   AAR42867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHUNG 1
                                                                                                                                                                                                      Similarity
                                                                                                                                                        EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
                                                                                                                                                                                                                                        73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koh Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nake; saxatilin; anticoagulant; cytostatic; venom; anti-tumour;
aggregation; angiogenesis; salmosin; cytotoxicity.
                                  standard;
                                                                                            GISAGCPRNPFHA
                                                                                                                 GISAGCPRNPFHA 73
                                                                                                                                           EAGEECDCGSPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCN
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sohn
                                 protein;
                                                                                                                                                                                                   94.5%;
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                                                                                                                                                                                        Score 409; DB 5; I
Pred. No. 1.3e-29;
2; Mismatches 3;
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                                                                                                                                                                                                              Length 73;
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                                                                                                                                                                                        Gaps
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Best Local S
Matches 67
                 27-JAN-1989;
27-JAN-1989;
01-NOV-1989;
                                                                                                                                                                       25-MAR-2003
04-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of a polypeptide which inhibits platelet caused by ADP, collagen, thrombin, arachidonic acid and PAF. 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2003
11-MAY-1994
                                                                                           WO9008772-A.
                                                                                                              Synthetic
                                                                                                                                 Snake venom;
                                                                                                                                                  Platelet aggregation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide of specified aminoacid sequence - platelet aggregation caused by e.g. collagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ50394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1990;
20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platelet aggregation inhibitory peptide
                                                      27-JAN-1989;
                                                                         09-AUG-1990
                                                                                                                                                                                                    AAR06494;
                                                                                                                                                                                                                     AAR06494 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 33-35; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-348481/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP05255395-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition; ADP; collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                      468
                                                                                                                                                                                                                                                                                                           408
                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                 67;
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                                                                                                                                                                                                                                                                      GISAGCPRNPFHA 480
                                                                                                                                                                                                                                                                                                            EAGEECDCGSPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKKGTVCRIARGDDMDDYCN
                                                                                                                                                                                                                                                                                                                      EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                  thromboxan A2; thrombosis; anti-coagulant
                                                                                                                                                                      (revised)
(first entry)
                89US-00303585.
89US-00303590.
89US-00430313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90JP-00287116.
91JP-00026328.
                                                      89US-00303585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91JP-00256234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                        94.5%;
                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombin; arachidonic acid;
                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                Score 409; DB 2;
Pred. No. 6.5e-29;
4; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for inhibiting thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                 Length 480;
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RESULT 7
AAU75225
ID AAU75225
ID AAU75225
AC AAU7
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is deduced from the coding strand of a synthetic gene for a polypeptide inhibitor of platelet activation. The polypeptide is analogous to that obtd. from the venom of Agkistrodon p. piscivorus (North American Water Moccasin). The gene can be used to produce recombinant inhibitor or fusion proteins with eg. hirudin derivs. These can be used to decrease/ inhibit platelet aggregation and release in vivo or in vitro. Usual dose is 0.01-100 mg/kg body wt. The recombinant protein can also be used to coat the surfaces of invasive medical devices. It can also block stenosis and spasm at the site of thrombosis (by inhibiting the release of thrombosan A2). See also AAR06508. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albumin fusion protein; therapeutic protein; immune disorder; autoimmune disorder; blood-related disorder; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disorder; endocrine disorder; reproductive system disorder; gastrointestinal disorder; infectious disease; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pure platelet activation inhibiting polypeptide from snake venom - for preventing agglutination and release in vivo or vitro, and new recombinant dna encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maraganore J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU75225 standard; protein; 71
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                                                                                                                                           12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agkistrodon piscivorus protein #2 relating to albumin fusion proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU75225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ05730.
         Ballance
                                                                                                                                                                                                                                                              12-APR-2001; 2001WO-US012009
                                                                                                                                                                                                                                                                                                                                                                              WO200179271-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Agkistrodon piscivorus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum albumin; HSA; HA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                         PRINCIPIA PHARM CORP.
DELTA BIOTECHNOLOGY I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
      Sleep
                                                            BIOTECHNOLOGY LTD
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         Turner AJ,
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Pred. No. 5.7e-29;
5; Mismatches 2
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         Sadeghi H,
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         Prior CP
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The present invention relates to albumin fusion proteins comprising a CC therapeutic protein and albumin (e.g. human serum albumin (HSA or HA)). CC The albumin fusion proteins are useful for treating, preventing, or CC ameliorating various disorders. Such disorders include immune disorders, cameliorating various disorders. Such disorders include immune disorders, cardiovascular disorders, immune disorders, cardiovascular disorders, reproductive CC disorders, renal disorders, cardiovascular disorders, reproductive cyclem disorders, reproductive system disorders, gastrointestinal disorders, infectious disease, and CC wound healing. Therapeutic proteins can be stabilised to extend shelf CC life and/or retain the protein's activity for extended periods of time in CC solution, in vivo or in vitro by genetically or chemically fusing the cyclein to albumin or its fragment or variant. In addition the use of CC albumin fusion proteins reduces the need to formulate protein solutions CC with large excesses of carrier proteins to prevent loss of therapeutic CC proliferation) of human albumin-human growth hormone (HA-HGH) fusion compared to no activity of unfused hGH. The present sequence represents the excension of compared to no activity of unfused hGH. The present sequence represents in the sequence is given in the sequence listing but is not mentioned elsewhere in the sequence listing but is not mentioned elsewhere in the sequence listing but is not mentioned elsewhere.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New albumin fusion proteins with extended shelf life, useful for treating leukemia, warts, hepatitis, multiple sclerosis and AIDS, comprises therapeutic protein fused to albumin.
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Ś 밁 Ş 밁 Best Matches Query Match Local 60 61 GISAGCPRNPFH 1 EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 65; Similarity GISAGCPRNPFH Conservative 90.6%; 72 Score 392.5; DB Pred. No. 4e-28; Mismatches 1; <u>ن</u> Indels Length ۲. Gaps 60 59

Sequence 71

A

specification

RESULT 8 AAR06395 05-FEB-1990; EP382451-A. Trimeresurus albolabris Fibrinogen binding; inhibitor; platelet aggregation; thrombosis; Viper venom. 25-MAR-2003 13-DEC-1990 AAR06395; AAR06395 standard; protein; 73 AA. 07-FEB-1989; Albolabrin 16-AUG-1990 (revised) (first entry) 89US-00307642 90EP-00301181

(MERI ) MERCK & CO INC

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RESULT 9
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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide is prepd. from the venom of the viper T. albolabris or may be prepd. by genetic engineering or solid phase synthesis. It inhibits both fibrin binding to human platelets and fibrinogen- induced aggregation of human platelets. It is eliminated from the ciculation rapidly and is therefore useful in situations where a strong antithrombic action of short duration is neede, e.g. in surgery on peripheral arteries, in cardiovascular surgery and the interaction of platelets with artificial surfaces. See also AARO6389-97. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                 Platelet aggregation GP IIA; GP IIIA; hype
       Disclosure; Fig
                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                            Trigramin-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-248351/33
                                   Platelet
                                                                                                                     07-JUN-1989;
                                                                                                                                        07-JUN-1989;
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                                                                                                                                                          13-DEC-1990.
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                                                             1991-007159/01.
                        let aggregation inhibiting amino venom and inhibit fibrinogen bir
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platelets and inhibiting
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                                                                                                   GENENTECH INC
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                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
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                                                                                Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                (first
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Holt JC,
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                                                                                                                      89US-00362718
                                                                                                                                        89US-00362718.
       1:
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       91pp; English
                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%;
                                                                                                                                                                                                                         inhibitor; snake venom; fibrin
                                                                                                                                                                                                                                                                                                                                                                     73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rucinski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gould
                                                                                                                                                                                                                                                                                                     73
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Pred. No. 5.6e-28;
4; Mismatches 5;
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                        ino acid
binding
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                          to GP IIA-GP
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 73;
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RESULT 10
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Best Local
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25-MAR-2003
21-DEC-1994
                                    The sequences given in AAR53933-46 are disintegrin peptides. Disintegrin are low molecular weight proteins from the Viperidae family of snakes which bind integrin proteins similar to the endogenous messenger and structurally interactive molecules. Disintegrins are competitive inhibitors of biomolecules, such as fibrinogen, for integrin binding sites such as G pib/IIIa on human platelets. Disintegrins contain the tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can be used for the treatment and diagnosis of venous and arterial thrombi, pulmonary embodi and tumours or abscesses that have a thrombus component (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
                                                                                                                                                                                                                 Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) treatment and diagnosis of venous and arterial thrombi, pulmonary en and tumours or abscesses having a thrombus component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence was produced by recombinant techniques using a synthetic gene prepd. from 10 oligonuclectides based on the amino acid sequence determined by Edman degardation. The recombinant triggramin-gamma is used in treatment of hypercoagulation-related states. See also AAR10107-R10113
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                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                     Knight
                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rin; Viperidae; snake; integrin; inhibitor; fibrinogen; binding sites; GP IIb/IIIa; human; platelets; radiolab: t; diagnosis; venous; arterial; thrombi; pulmonary emboabscesses; thrombus component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                           field.)
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Pred. No. 5.6e-28;
4; Mismatches 5;
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Sequence 73

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                                                CC ontrast agent for diagnostic imaging or a target composition which CC comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination CC with (iii) a targeting ligand (T1). The targets cells or receptors with (iii) a targeting ligand (T1). The targets cells or receptors composition of polymer and (iii) a gas, in combination CC with (iii) a targeting ligand (T1). The targets cells or receptors and CC the glycoprotein GPID/IIa receptor. Also claimed are: a composition comprising (i) - (iii) and an agreeous carrier; a composition stargeted vesicle composition comprising a fluorinated gas and a targeting CC ligand (T1') which targets tissues or receptors; a formulation for CC therapeutic or diagnostic use comprising (i) - (iii) and a bioactive agent; and a method for providing an image of an internal region of a patient, CC or for diagnosing the presence of diseased tissue, comprising; (a) composition of a composition as above; and (b) scanning the patient CC using ultrasound to obtain a visible image of the region or diseased tissue. The methods and compounds are useful for imaging or diagnosing the presence of diseased tissue, especially myocardial, endothelial or epithelial tissue but also gastrointestinal and cardiovascular regions. CC in particular the ligand targets regions of arteriosclerosis. Stabilised CC vesicles are particularly useful for perfusion imaging. The vesicles may CC also be used to deliver active agents to an intended target such as CC tissue or a receptor, and ultrasound can then be used to promote rupture of the vesicles and release a bioactive or diagnostic agent
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01-MAY-1996;
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96US-00640464.
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Pred. No. 5.6e-28;
4; Mismatches 5
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RESULT 12
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                                 The invention relates to a method of: (A) delivering a bioactive agent CC (BA) to a patient by: (a) administering a composition comprising: (i) an CC anionic lipid (AL); (ii) a cationic counter ion (CCI); (iii) a lipid (CC covalently bonded to a polymer (LDP), and (iv) BA, and (b) applying CC therapeutic ultrasound to facilitate delivery of BA in a desired region; CC (B) delivering a BA to a patient, comprising administering a composition (CC); a counter ion (CI), LDP, BA and (CC cargeting ligand (TL); (C) providing an image of an internal region of a gatient, comprising: (a) administering a composition comprising CL, CI CC and LDP of the composition in (B), and (b) scanning the patient using CC diagnostic imaging, to give visible images of the region, and (D) (CC) contrast agent comprising components as in (Ca). The compositions/processes described above may be used in drug delivery, therapeutic imaging and diagnostic imaging. This compense of a targeting ligand designated
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Best Local :
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06-MAY-1997;
18-JUN-1997;
02-JUL-1997;
08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bioactive agent, anionic lipid; cationic counter ion; lipid covalently bonded to a polymer; ultrasound; charged lipid; targeted drug delivery; diagnostic imaging; targeting ligand; GPIIbIIIa receptor; diagnosis; vascular thrombosis; clot.
                                                                                                                                                                                                                                                                                               Processes for drug delivery, therapeutic comprises use of compositions comprising lipid covalently bonded to polymer.
                                                                                                                                                                                                                                                                                                                                                                                      Unger
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                                                                                                                                                                                                                                                                       Disclosure; Page 68; 167pp; English
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EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN

EAGED CD CGS PAN P CCDAAT CKLLPGAQ CGEGL CCDQCS FMKKGT I CRRARGDDLDDYCN

60

Query Match Best Local S Matches 64

Similarity

90.3%;

Score 391; DB Pred. No. 5.6e 4; Mismatches

DB 2;

Length 73;

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GISAGCPRNPLHA

AAB20598 standard; peptide;

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Albolabrin targeting

ligand peptide

12-DEC-2000

(first entry)

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S
                                                                                                        Matches
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Best Local
                                                                                                                                           The present invention describes an ultrasound method comprising: (i) administering a targeted vesicle composition (A); and (ii) scanning the subject by exposure to a first type of ultrasound energy and then interrogating with a second type of ultrasound energy. (A) consists of a vesicle comprising a lipid, protein or polymer, encapsulating a gas, in combination with a targeting ligand. The method is used to detect: (I) a thrombus (particularly old or echogenic); (II) a low concentration of vesicles; or (III) vesicles targeted to endothelial tissue, particularly those containing integrins associated with malignancy or inflammation in early or small lesions, e.g. atheroselerotic plaque or ovarian, endometrial or other carcinomas. The method increases the signal from microbubbles and reduces background noise. The present sequence represents a targeting ligand peptide which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                    Ultrasound method, useful for diagnosis of uses different types of energy for priming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2000; 2000WO-US002620
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 70; 211pp; English.
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EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
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EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN

Query Match Best Local S Matches 64

Similarity

90.3%;

Score 391; DB Pred. No. 5.6e 4; Mismatches

DB 5;

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RESULT 14
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                           This invention relates to a novel targeted compound having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand. The cinvention also comprises a target vesicle composition comprising lipid, protein or polymer gas filled vesicles in an aqueous carrier, a method comprises a thrombus in a region of a patient involving administering to the patient a target vehicle composition and scanning the region (preferably cardiac region) with diagnostic imaging (preferably cardiac region) with diagnostic imaging (preferably composition and scanning the region of diagnostic ultrasound) and a method for lysing a thrombus in a blood vessel. The invention also comprises a method for providing an image of an internal region of a patient which can be used to obtain a visible image of a region (preferably arteriosclerosis, atherosclerotic plaque, infarcted myocardium or a cancer cell) and a method for diagnosing the presence of disease tissue in a patient involving administering a target vehicle composition and scanning the patient using ultrasound to obtain a visible image of the region. The methods of the invention may be used for imaging a thrombus in a region of a patient using ultrasound to obtain a visible image of the region. The methods of the invention may be used for the invention are easily synthesised and have diagnostic efficacy, over prior art methods. The present sequence represents a glycoprotein GPIIbIIIa receptor targeting ligand albolabrin used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New targeted compound useful in target vesicle composition for imaging thrombus in a region of a patient has a combination of hydrophobic compound, hydrophilic polymer and targeting ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 68; 206pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-2000; 2000US-00699679,
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A.
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Targeting ligand peptide; imaging; ultrasound; vesicle; tumour; myocardial; endothelial; epithelial; glycoprotein GPIIbIIIa receptor; detection; thrombus; integrin; malignancy; inflammation; lesion; atherosclerotic plaque; carcinoma.

Unidentified

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01-MAY-1996;
06-JUN-1996;
06-FEB-1998;
22-DEC-1998;
                        palmitoylglycerophosphoethanolamine and phosphatidic acids. The method scanning involves exposing the pattent to a first ultrasound energy having a first insonation frequency to cause the vesicle to oscillate, and then subsequently, while the vesicle is oscillating, exposing the patient to a second ultrasound energy having a second insonation frequency that is different from the first insonation frequency, and detecting the reflected ultrasound signal. The method is useful for ultrasound diagnosis, for detection of a thrombus or enhancement of thrombus (e.g. old or echogenic thrombus) and for detecting vesicles
                                                                                                                                                                                                                                                                            The present invention relates to a novel ultrasound method which involves administering to a patient a targeted vesicle composition which comprises vesicles encapsulating agas, in combination with a targeting ligand, and scanning the patient using dual frequency ultrasound insonation. The vesicles themselves comprise a lipid, protein or polymer, and are selected from liposomes and micelles. The vesicles may comprise a phospholipid selected from diolecylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine, N-succipylphosphatidylcholine, dipalmitoylphosphatidylethanolamine, N-succipyldhosphatidylethanolamine, N-s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ultrasound diagnosis, by administering targeted vesicle composition with vesicles encapsulating gas, in combination with targeting ligand, to a patient, and scanning patient by dual frequency ultrasound insonation.
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thrombus (e.g. old or echogen: targeted to epithelial cells,
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96US-00660032.
98US-0073913P.
98US-00218660.
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                                                                                                                                                                                                                                         endothelial tissue including integrins associated with malignancy or inflammation. The method is also useful for diagnosing the presence or absence of diseased tissue in a patient, and for imaging one or more regions of a patient, such as for providing images of the heart, gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent targeting ligands that may be used in the method of the present invention
                                                                                                                                                                                                          Sequence 73
61
                               61 GISAGCPRNPFHA 73
                                                                     \vdash
                                                                                           1 BAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
                                                                                                                                      64; Conservative
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 GISAGCPRNPLHA
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 73
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Pred. No. 5.6e-28;
4; Mismatches 5
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Search completed: December Job time : 117 secs 2004, 21:35:44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N Geneseq 23Sep04:*

1: geneseqn1980s:*
2: geneseqn1900s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
5: geneseqn2002as:*
7: geneseqn2003bs:*
8: geneseqn2003as:*
11: geneseqn2003ds:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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1 ggagaagaatgtga
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Match Length
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Gapop 10.0 , Gapext 1.0
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geneseqn2003ds:*
geneseqn2004s:*
       GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
    AAQ50385
AAQ44932
AAQ50390
AAQ50386
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ACC47594
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                                                                                                                                                                                                                                                                                                                                       AAD31060
ACC44733
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AAD07386
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Compugen Ltd.
Aad31060 Agkistrod
Acc44733 Agkistrod
Aag50394 Platclet
Aag50394 Platclet
Aaz55609 Korean sn
Aaz54821 Scistrod
Abs54622 Disintegr
Acc47594 Disintegr
Aag50357 pAGalpha2
Aag50358 Platclet
Aag44932 pAGalpha1
Aag50390 Platclet
Aag4932 pAGalpha1
Aag4934 Platclet
Aag44934 Platclet
Aag44936 Platclet
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Aag44939 pAGalpha8
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ADF66009	ABK14952	σ	ABK10649	ABX93010	ABX93715	9	AAQ25314	ω	16	ABK10644	63	73	ABS54624	4	ABK10642	338	AAQ50388	93	Ψ	AAQ50387	φ	39	- 1
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Adf66009	<b>bk14952</b>	Abk10643	bk10649	bx93010	bx93715	ac85063	Aaq25314	aq25315	aq10160	bk10644	bk10638	aq05730	Abs54624	Abk10648	77	389	88	937	335	Aaq50387	aq44936	aq50392	i
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## ALIGNMENTS

RESULT 1 AAD31060

29-AUG-2003 07-AUG-2003 18-JUN-2002

(revised)
(revised)
(first entry)

AAD31060;

AAD31060 standard; cDNA; 213 BP.

Korean snake; saxatilin; anticoagulant; cytostatic; venom; anti-tumour; platelet aggregation; angiogenesis; cytotoxicity; ss.

Agkistrodon saxatilis emelianov saxatilin cDNA.

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Gloydius halys.
                  WPI; 2002-241903/29.
P-PSDB; AAE19787.
                                                                                 26-JUL-2000; 2000WO-KR000809
                                                                                              21-FEB-2002.
                                    Hong S,
                                                                    26-JUL-2000; 2000WO-KR000809
                                                                                                           WO200214488-A1
                                                (CHUN/) CHUNG K. (KIMD/) KIM D.
                                    Koh Y,
                                                                                                                     /*tag= a
/product= "Saxatilin protein"
/product= "Saxatilin protein"
/transl except= (pos:1. .3, aa:Glu-Ala-Gly)
/note= "Deletion of 6 bases alters the reading frame; CDS
does not include start and stop codon"
                                                                                                                                                                   Location/Qualifiers
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New cDNA encoding Saxatilin protein derived from venom of Korean snake Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation

agent and anti-tumor agent

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RESULT 2
ACC44733
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Matches 213
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                                                    Lipoplex useful for inhibiting growth of cancer cells, and or preventing cancer, comprises a cationic liposome and an vector containing the saxatilin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agkistrodon saxatilis; saxatilin; anti-cancer; cancer; disintegrin; tumour; lipoplex; cancer growth inhibition; cationic liposome; cytostatic; gene therapy; gene; ss.
  Claim 1; Page 20; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2001; 2001WO-KR001461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gloydius halys.
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29-MAY-2003
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Similarity 100.0%; Pred. No. 1.5e-62;
13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                        Park Y,
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(first entry)
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a lipoplex for inhibiting cancer growth comprising a cationic liposome and an expression vector containing a saxatilin gene having a sequence of 222 base pairs (bp), given in ACC44733. Also described is a method for inhibiting cancer growth by using a saxatilin gene, which comprises: (a) mixing cholesterol with DOTAP, suspending the mixture in aqueous medium to prepare cationic liposome, and introducing saxatilin gene to eukaryotic vector; (b) mixing the cationic liposome and expression vector in aqueous medium and homogenising to prepare lipoplex; and (c) introducing the lipoplex to a cancer tissue. Saxatilin is a disintegrin gene which has cytostatic activity and can be used in gene therapy. The lipoplex is useful for inhibiting growth of cancer cells, and for treating or preventing cancer. (Updated on 27-OCT-2003 to standardise OS field)
Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                          WPI; 1993-348481/44.
P-PSDB; AAR42867.
                                                                                                                   26-OCT-1990;
20-FEB-1991;
                                                                                                                                                             03-OCT-1991;
                                                                                                                                                                                             05-CCT-1993.
                                                                                                                                                                                                                         JP05255395-A
                                                                                                                                                                                                                                                                                                             Gloydius halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                           Inhibition; ADP; collagen; thrombin; arachidonic
                                                                                                                                                                                                                                                                                                                                                                      Platelet aggregation inhibitory peptide
                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2003
11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ50394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ50394 standard; cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 222 BP; 59 A; 47 C; 68 G; 48 T; 0 U; 0 Other;
                                                                                      (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAGAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
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(first entry)
                                                                                                                   90JP-00287116
91JP-00026328
                                                                                                                                                               91JP-00256234
                                                                                                                                                                                                                                                                    Location/Qualifiers 10. .1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA; 1558 BP
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Pred. No. 1.5e-62;
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                                                                                                                                                                                                                                                                                                                                             acid; PAF;
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RESULT 4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that encoding a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                  Gloydius halys
                                                                                                                                                                                                                                                                                                                        Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;
metastasis; cancer; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1558 BP; 468 A; 310 C; 362 G; 418 T; 0 U; 0 Other;
 This sequence
Korean snake,
                                                                                                         Ki m
                                                                                                                                                 23-JUN-1998;
04-JUN-1999;
                                                                                                                                                                                                                         EP967276-A2
                                                                                                                                                                                                                                                                  Key
mat_peptide
                                                                                                                                                                                                                                                                                                                                                       Korean snake venom salmosin cDNA.
                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003
27-MAR-2000
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                                                                                                                                                                                 23-JUN-1999;
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                                                                                                                             (KIMD/) KIM D.
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DB; AAY58231.
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                                                    polypeptides used for antitumor therapy
                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGAGAAGATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
                                                                                                      Chung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 33-35; 50pp; Japanese
                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGGAACAGTATGCCGGATAGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA
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                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
represents cDNA encoding the 7.5 kD salmosin Agkistrodon halys brevicaudus. Salmosin is a
                                                                                                       <u>꾸</u>
                              14; 24pp; English
                                                                                                                                                 98KR-00023778.
99KR-00020579.
                                                                                                                                                                                 99EP-00304935
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                         /*tag= a
                                                                                                                                                                                                                                               /product= "Korean snake salmosin"
                                                                                                      Kang
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Pred. No. 3e-
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protein of a disintegrin,

29-SEP-1999; 06-APR-2000

99WO-US022608

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CC integrin alpha-v-beta-3 can suppress tumour induced angiogenesis.

CC integrin alpha-v-beta-3 can suppress tempour induced angiogenesis.

CC integrin alpha-v-beta-3 can suppress tempour reduction of the inhibition or reduction of tumour cell angiogenesis, the inhibition or reduction of tumour cell angiogenesis, the inhibition of metastatic tumour growth. Nucleotides encoding salmosin may be used in gene therapy applications. Many types of cancer may be treated with salmosin or nucleotides encoding it, including leukaemia and cancers of the breast, ovary, uterus, skin, lung, laryxx, colon, pancreas, testis, liver, brain, muscle and bone. (Updated on 15-SEP-2003 to standardise OS field)
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Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Southern copperhead snake; venom; contortrostatin; disintegrin; cytostatic; antiproliferative; thrombolytic; cerebroprotective; antiaggregant; antiarteriosclerotic; antianginal; cardinat; metastasis; thromboembolism, stroke; arteriosclerosis; atherosclerosis; embolism; aneurism; angina; myocardial infarction; integrin; ss.
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                                                                                                                                                                                                                                                polyA_site
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                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agkistrodon contortrix.
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ilarity 95.3%;
Conservative
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Pred. No. 4.7e-57;
0; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of claimed DNA encoding the Southern CC copperhead snake venom disintegrin, contortrostatin (see AAY79413), a CC protein that inhibits the interactions between integrins and their CC protein that inhibits the interactions between integrins and their CC protein that inhibits the interactions between integrins and their CC amplification using primers (see AAZ94882-83) based on a conserved region CC of disintegrins. Contortrostatin precursor protein includes a pro-protein CC and a disintegrin region which includes an RGD loop that acts as an CC integrin antagonist. DNA molecules consisting of nucleotides 1341-1535 (encoding the disintegrin), 657-1316 (metalloproteinase), 87-656 (proceding the disintegrin), 657-1316 (metalloproteinase), 87-656 (proceding the disintegrin) regeators protein) of the present sequence CC are also claimed. These can be used in the recombinant production of CC pharmaceutical compositions for treating diseases associated with an CC integrin binding to an integrin receptor, especially to inhibit platelet CC aggregation, tumour metastasis, angiogenesis, neovascularization, cell CC adhesion, invasiveness, or growth (all claimed). The proteins are also CC useful for treating a thrombotic disorder, e.g. preventing arterial, CC venous, and microvascular thrombotis and thromboembolism, stroke, CC transient ischaemic attacks, arteriosclerosis, atherosclerosis, pulmonary CC embolism, aneurism, angina and myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 199;
Southern copper head snake; contortrostatin; CN; cytostatic; osteopathic; vulnerary; disintegrin; platelet aggregation; neovascularisation; tumour; integrin; angiogenesis; metastasis; invasiveness; growth; metastasis; metastasis; copperations are carcinoma; sarcoma; therapy; thrombotic disease; osteoporosis;
                                                                                                                                                                                                                             AAD07386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2029 BP; 630 A; 433 C; 423 G; 543 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Fig 3A-D; 81pp; English
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                                                                                                    Agkistrodon contortrix contortrostatin (CN) cDNA.
                                                                                                                                               04-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             el proteins and polynucleotides representing contortrostatin useful inhibiting platelet aggregation, tumor metastasis and growth.
                                                                                                                                                                                                                                                                                                                                                                                                              1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGAAGAATGTGACTGTGGGGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                       TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                GAAGGAACAGTATGCCGGAGAGCAAGGGGTGATGACCTGGATGATTACTGCCAATGGCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGACAACAGGGTCACAGTGTGCAGATGGACTGTGTTGTGACCAGTGCAAATTTATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGACCAGGGGGGAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGAAGAAAGTGACTTTGACGCTCCTGCAAATCCGTGCTGCGATGCTGCAACATGTAAA
                                                                                                                                                                                                                                                                                                                               TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC 1535
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                                                                                                                                                                                                                             cDNA; 2029
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Pred. No. 1.8e-54;
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                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                    Matches 199;
                                                                                                                                                                                                                                        The present sequence is southern copper head snake cDNA encoding contortrostatin (CN) protein. CN, a homodimeric disintegrin binds to integrin alphaybeta5 and induces alphaybeta3-mediated tyrosine phosphorylation of CAS and FAK in tumour cells. CN is useful for modulating the adhesion, mothlity, and invasiveness of integrin expressing cells, preferably tumour cells and for inhibiting the adhesion of integrin expressing cells to vitronectin. The pharmaceutical composition comprising CN is useful for inhibiting platelet aggregation, neovascularisation, angiogenesis, tumour metastasis, invasiveness or growth, for inhibiting metastasis in melanoma, caracinoma and sarcoma patients. It is also useful for treating thrombotic diseases,
                                                                                                                                                                                                   Sequence 2029 BP; 630 A; 433 C; 423 G; 543 T; 0 U; 0 Other;
                                                                                                                                                                                                                               osteoporosis, and
                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 3; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         Homodimeric disintegrin useful for modulating the adhesion, motility, invasiveness of integrin expressing tumor cells.
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08-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WC200141791-A1
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                                                                                                                  1 GGAGAAGAATGTGACTGTGGGGGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAA
                                                                                                                                                                 Similarity
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                 GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
                                                 CTGACAACAGGGTCACAGTGTGCAGATGGACTGTGTTGTGACCAGTGCAAATTTATGAAA
                                                                  CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA
                                                                                                   GGAGAAAGTGACTTTGACGCTCCTGCAAATCCGTGCTGCGCATGCTGCAACATGTAAA
                                                                                                                                                    Conservative
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2000US-00591552.
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/note= "Encodes I
1539. .2029
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1988. .
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                                                                                                                                                                                                                              wound healing in mammals
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Pred. No. 1.8
                                                                                                                                                    ed. No. 1.8e-54;
Mismatches 14
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TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC

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             The invention relates to a new isolated polypeptide, which is a disintegrin protease designated ZSNX16 from Sistrurus miliarius, comprising an integrin binding region (designated ZSNX16-br) or a zinc-binding motif (designated ZSNX16-zbm). Also included are the nucleic acid encoding ZSNX16, producing anti-ZSNX16 attransformed cultured cell expressing ZSNX16, producing anti-ZSNX16 ibr and ZSNX16-zbm domains. The polypeptide is useful as a tool for investigating cell-matrix and cell-cell interactions, for studying cell proliferation or differentiation in human tissues, for studying immune recognition, fertilisation, growth control or angiogenesis, for identifying inhibitors of its activity, or themotherapy agents or small molecules). The ZSNX16 polypeptide is also need to the control of agents or small molecules. The ZSNX16 polypeptide is also
                                                                                                                                                                                                                                                                          New disintegrin protease (designated ZSNK16) homolog polypeptides, useful in modulating cell-cell interactions, delivering therapeutic agents, or is replacement therapy for e.g. fertility, coagulation, thrombosis or
                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamete maturation; i epithelial disorder.
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                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                      OMYZ)
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DB; ABG70857.
                                                                                                                                                                                                                                                                                                                                                                                      Sheppard PO
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py agents or small molecules). The ZSNK16 polypeptide is also replacement therapy for disorders associated with cell-cell
                                                                                                                                                                                                                                  Page 70-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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88. .141
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142. .648
/*tag= c
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Best Local S
Matches 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions, e.g. fertility, gamete maturation, immunology, coagulation, thrombosis, trauma or epithelial disorders. The polypeptide is also useful in the development of antithrombotic and antimetastatic agents due to their anti-adhesive, anti-migration of certain tumour cells, and anti-angiogenesis activities. The antibodies to the ZSNK16 polypeptide are useful for tagging cells that express ZSNK16, for isolating ZSNK16 by affinity purification, for detecting or quantifying soluble ZSNK16 as marker of underlying pathology or disease, or for screening expression libraries. The present sequence encodes ZSNK16
                                                                                                                                                                                                                                                                                                                                                                           Disintegrin-gamma; cysteine-rich; RGD motif; integrin antagonist; inhibition; vascularisation; tumour growth; tumour metastasis; cancer; cytostatic; gene; ss.
                                                     08-FEB-2002; 2002CN-00103679
                                                                                  08-FEB-2002; 2002CN-00103679
                                                                                                                                         CN1374318-A.
                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disintegrin-gamma cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC47594 standard;
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                                                                                                             16-OCT-2002.
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                                                                                                                                                                              /partial
/product= "Disintegrin-gamma"
/product= "No start codon given in the specification"
/transl_except= (pos:16...18, aa:Tyr)
/transl_except= (pos:14...18, aa:Tyr)
/transl_except= (pos:124...126, aa:Gln)
/transl_except= (pos:127...129, aa:Gln)
/transl_except= (pos:127...129, aa:Gln)
/note= "The above translation exceptions relate on."
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92.0%;
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Pred. No. 8.1e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2102;
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RESULT 9
AAQ50347
ID 0475
AC 1475
AC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAGalpha201 platelet aggregation inhibitory polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and nucleic acids encoding it (ACC47594). Disintegrin-gamma is cysteinerich, contains an RGD integrin-binding motif, and acts as an integrin antagonist. Disintegrin gamma may be used to inhibit integrin-mediated activities such as vascularisation, and tumour growth and metastasis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a disintegrin-gamma protein (ABP97447, ABP97448) and nucleic acids encoding it (ACC47594). Disintegrin-gamma is cysteine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 7 (Disclosure); 12pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New natural dissociation essence gamma gene and antineoplastic active polypeptide dissociation essence-gamma, useful as a fusion body antagonist to inhibit vascularization, tumor metastasis and tumor gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-168400/17.
P-PSDB; ABP97447, AB
                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP05255395-A
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11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ50357;
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Example; Fig 3; 50pp;
                                                 Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                        WPI; 1993-348481/44.
P-PSDB; AAR42887.
                                                                                                                                                                                                                                                                             26-OCT-1990;
20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                           03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ50357 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents cDNA encoding disintegrin-gamma
                                                                                                                                                                                                                   (TAKE ) TAKEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGAAGAATGTGACTGTGGCGCTCCTGCAAAATCCGTGCTGCGATGCTGCAACCTGTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAACCAAGGAGCACAGTGTACAGCAGGACCGTGTTGTGACCAGGGCAGATTTAAGGAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTTGTGACCAGTGCAGATTTATGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGGAACAATATGCCCGGAGAGCAAGAGGTGATGACCTGGATGATTACTGCAATGGCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCTGACTGTCCCAGAAATCCCTACCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP; collagen; thrombin; arachidonic acid; PAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                          90JP-00287116.
91JP-00026328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blomhoffi
                                                                                                                                                                                                                                                                                                                                                           91JP-00256234.
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                                                                                                                                                                                                                         UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%;
88.7%;
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Pred. No. 2.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 222;
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4 GAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG

Matches 161; Query Match Best Local (

Similarity

71.9%;

Conservative

0,

Score 153.2; DB 2 Pred. No. 4.2e-42; 0; Mismatches 13

DB 2;

Length

Indels

0

Gaps

0

63

Sequence 174 BP; 51 A; 31 C; 55 G; 37 T; 0 U; 0 Other;

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RESULT 10
AAQ44933
ID AAQ44933
ID AAQ44
AC AAQ44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of pAGalpha201 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
                                                                                       The sequence is that of pAGalpha2-101 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-
                                                                                                                                                                                                                                                                                           Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-CCT-1990;
20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2003
11-MAY-1994
                                                                                                                                                                                                                                      Example; Fig 13; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloydius halys blomhoffi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAGalpha2-101 platelet aggregation inhibitory polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ44933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ44933 standard; cDNA; 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                              to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                     AAR46947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGACTGCGACTGTGGCTCCTGGAAATCCGTGCTGTGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAACAGTATGCCGGATAGCAAGGGGTGATGACATGGATGATTACTGCAATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90JP-00287116
91JP-00026328
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93.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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RESULT 12
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ID AAQ44
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AAQ50385
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                                                                                                                                                                                 Query Match
Best Local S
Matches, 161
                                                                                                                                                                                                                                            The sequence is that encoding a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                       Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP05255395-A.
         AAQ44932
                                                                                                                                                                                                                                                                                    Example; Page 27; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gloydius halys blomhoffi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet aggregation inhibitory peptide
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11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ50385 standard; cDNA to
                                                                                                                                                                                                                         Sequence 174 BP; 51
                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition; ADP; collagen; thrombin; arachidonic
                                                                                                                                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND
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DB; AAR42858.
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                                                                                                                                         Н
                                                                                                                                                            41
                                                                                                                                                                                            Similarity
         standard; cDNA;
                                                                        GGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGC 177
                                                                                                              AGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAAGAA
                                                                                                                                                         GAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATTACTGCAATGGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGACTGCGACTGTGGCTCTCTGGAAATCCGTGCTGATGCTGCAACCTGTAAACTG
                                                                                                                                          GAGGACTGCGACTGTGGCTCTCCTGGAAATCCGTGCTGTGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAACAGTATGCCGGATAGCAAGGGGTGATGACATGGATGATTACTGCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACAAGGAGCACAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTAAGAAAAAA
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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91JP-00026328.
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                                                                                                                                                                                                                         A; 31 C; 55 G; 37 T; 0 U; 0 Other;
                                                                                                                                                                                          71.9%;
         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA;
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                                                                                                                                                                                 Score 153.2; DB 2;
Pred. No. 4.2e-42;
0; Mismatches 13;
         ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid;
                                                                                                                                                                                                    Length 174;
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RESULT 13
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Best Local Sim
Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of pAGalpha1-101 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-2003
11-MAY-1994
                        24-OCT-2003
11-MAY-1994
                                                               AAQ50390;
                                                                                        AAQ50390 standard;
                                                                                                                                                                                                                                                                                                                                                                Sequence 174 BP; 50 A; 31 C; 54 G; 39 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-348481/44.
P-PSDB; AAR46946.
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20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pAGalpha1-101 platelet aggregation inhibitory polypeptide.
Platelet aggregation inhibitory peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 12; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloydius halys blomhoffi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibition;
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                                                                                                                                                                              124
                                                                                                                                                       121
                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                            4 GAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                          GGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATTACTGCAATGGC 177
                                                                                                                                                                                                                                  AGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAAGAA 123
                                                                                                                                                       GGAACAGTATGCCGGATAGCAAGGGGTGATGACATGGATGATTACTGCAATGGC
                                                                                                                                                                                                        AGACAAGGAGCACAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTTTAAAAAAA
                                                                                                                                                                                                                                                           GAGGACTGCGACTGTGGCTCTCCTGGAAATCCGTGCTGTGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP; collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                        (revised)
(first entry)
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91JP-00026328.
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                                                                                         CDNA
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                                                                                         mRNA;
                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                             Score 151.6; DB 2
Pred. No. 1.5e-41;
0; Mismatches 14
                                                                                         174
                                                                                         ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arachidonic
                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid; PAF;
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                        174;
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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                             60
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                                                                                                                                                                                                                                                                                     63
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Gloydius halys blomhoffi

Inhibition; ADP; collagen;

thrombin; arachidonic

acid;

JP05255395-A. 05-OCT-1993.

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AAQ50384
ID AAQ50
XX AAQ50
AC AAQ50
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Best Local Similarity 92.0
Matches 160; Conservative
                                                                                                                                                                                                                                                                                     26-OCT-1990;
20-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                              03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP05255395-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Platelet aggregation inhibitory peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 174 BP; 50 A; 32 C; 55 G; 37 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that encoding a polypeptide which inhibits aggregation caused by ADP, collagen, thrombin, arachidonic (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1990;
20-FEB-1991;
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                                                                            Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition; ADP; collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2003
11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ50384 standard; cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR42863.
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                           Example; Page 27; 50pp; Japanese
                                                                                                                                                          WPI; 1993-348481/44.
P-PSDB; AAR42857.
                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1993
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                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGAATGTGACTGTGGCGCTCCTGCAAATCCGTGCTGCGATGCTGCAACCTGTAAACTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAACAGTATGCCGGATAGCAAGGGGTGATGACCTGGATGATTACTGCAATGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACAAGGAGCACAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTAAGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGACCAGGGGGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAAGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGACTGCGACTGTGGCTCCTGGAAATCCGTGCTGTGATGCTGCAACCTGTAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised) (first entry)
                                                                                                                                                                                                                                                                                     90JP-00287116.
91JP-00026328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blomhoffi
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91JP-00026328.
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                                                                                                                                                                                                                                                                                                                                                                 91JP-00256234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombin; arachidonic acid; PAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA; 174 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 151.6;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           platelet
acid and
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Best Local Similarity
Matches 160; Conserv
                                                                                                Matches 159;
                                                                                                                                                                                                                                                     The sequence is that of pAGalpha3-101 cDNA which comprises a polypeptide isolated from Agkistrodon halys blomhoffi. It was used in the isolation and prodn. of a polypeptide inhibiting platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and PAF. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that encoding a polypeptide which inhibits platelet aggregation caused by ADP, collagen, thrombin, arachidonic acid and (Updated on 24-OCT-2003 to standardise OS field)
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P-PSDB; AAR46948.
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11-MAY-1994
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                                                                                                                                                                                                      Sequence 174 BP; 49 A; 32 C; 54 G; 39 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 14; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide of specified aminoacid sequence - used for inhibiting platelet aggregation caused by e.g. collagen, thrombin, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1990;
20-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibition; ADP; collagen; thrombin; arachidonic acid; PAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pAGalpha3-101 platelet aggregation inhibitory polypeptide
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                                                                                                                            Similarity
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91JP-00026328.
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Search completed: December 3, 2004, 18:47:15 Job time : 409 secs

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Result
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-264-101-1

US-08-265-243-7

PCT-US95-07295-1

US-08-786-225-7

PCT-US95-07295-7

PCT-US95-07295-7

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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5182260
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US-10-17-308- US-10-17-308- US-10-17-308- US-10-17-308- US-10-17-308- US-10-18-836-442- US-08-836-442- US-09-280-116- US-09-548-797B US-09-548-797B US-09-632-098- US-10-177-308- US-10-177-308- US-10-177-308- US-09-548-797B US-09-632-098- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308- US-10-177-308-
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## ALIGNMENTS

RESULT 1 US-09-776-268A-3

Sequence 3, Application US/09776268A Patent No. 6537551

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GENERAL INFORMATION:
APPLICANT: KIM, DOO-Sik
APPLICANT: CHUNG, KWANG HOE
APPLICANT: CHUNG, KWANG HOE
APPLICANT: CHUNG, KWANG IN-Cheol
TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SAL
FILE REFERENCE: 0136/1F733-US1
CURRENT APPLICATION NUMBER: US/09/776,268A
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: US 09/335,088
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 98-23778
PRIOR APPLICATION NUMBER: KR 98-23778
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 7
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Best Local Sim
Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 222
                                                                      127
 187
                                    181
                                                                                                        121
                                                                                                                                            67
                                                                                                                                                                        61 CTGAGACCAGGGGGCGCAGTGTGCAGAAGGACTGTGTGACCAGGTGCAGATTTATGAAA
                                                                                                                                                                                                                                       1 GGAGAAGGAATGTGACTGTGGCGCCTCCTGCAAATCCCGTGCTGCCGATGCTGCAACCTGTAAA
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                                                                                                                                                                                                                                                                                                        Similarity
                      TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC
                                                                                                  GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATTACTGCAATGGCATA
                                                                      GAAGGAACAATATGCCGGAGAGCAACGCGTGATGACCTGGATGATTACTGCAATGGCATA
                                                                                                                                            CTGAGACAAGGAGCACAGTGTGCAGAAGGACTGTGCTGACCAGTGCAGATTTATGAAA
rerectedereceagaaarecerrecarece
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Pred. No. 2.5e-57;
0; Mismatches 12
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                                    213
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RESULT 2 US-09-460-295B-1 ; Sequence 1, Application US/09460295B

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Best Local S
Matches 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08745603
Patent No. 5814609
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2029
TYPE: DNA
ORGANISM: Agkistrodon contortrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN ((N) AND METHODS FOR
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338G3/09801388
CURRENT APPLICATION NUMBER: US/09/460,295B
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ. ID NOS: 15
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO: 1:
.SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Francis S. Mar)
APPLICANT: Qing Zhou
TITLE OF INVENTION: COMPO:
TITLE OF INVENTION: ITS U:
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Robert Berliner
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 1920
TELECOMMUNICATION INFORMATION:
TELECHONE: 213/977-1001
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,603
                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1443
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                                                                                                                                                                                                                                                                                                                                 90012-2628
                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Robbins, Berlin
F: 201 No. 5814609th
Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGACAACAGGGTCACAGTGCAGATGGACTGTGTTGTGACCAGTGCAAATTTATGAAA 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCTGGCTGTCCCAGAAATCCCTTCCATGCC
                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Francis S. Markland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOSITIONS CONTAINING A DISINTEGRIN AND METHODS ITS USE IN PREVENTING METASTASIS AND OTHER CONDITI
                                                                                                                                                                                                                                                                                                                                                                                                             Berliner & Carson
4609th Figueroa Street,
                                                                                                                                                                                                                   US/08/745,603
                                                                                                1920-338C1
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Pred. No. 8.8
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Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                 Suite
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PILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
PILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
PILING DATE: 27-JAN-1989
SEQ ID NO:22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
5182260-22
;PATENT NO. 5182260
;PATENT NO. 5182260
; PATENT NO. 5182260
; PATENT NO. 5182260
; TITLE OF INVENTION; DNA SEQUENCES ENCODING SNAKE VENOM
;INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
;THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION NUMBER: US/08/430,313
; APPLICATION NUMBER: US/08/430,313
RESULT 5
5182260-1
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                     Matches 157;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 911 base pairs (111 amino acids)
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                   181
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                                                                                                                                                                                                                                                        ggagaagaargragcrgrgggggcrccrgcaaarccgrgcrgcgargcrgcaaccrgraaa
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                                                                                 rcrecreccioreccaeaarecerreca 209
                                                                                                                GAAGGTACCGTTTGCCGTCGTGCTCGAGGTGACGACGTTAACGACTACTGCAACGGTATC
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                                                                                                                                          GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA
                                                                                                                                                                        CTTCGTCCGGGTGCACAGTGTGCAGAAGGTCTGTGCTGCGACCAGTGCAAATTCATGAAA
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                                                         TCTGCAGGTTGCCCGCGTAACCCGTTCCA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTGTTGTGACCAGTGCAAATTTATGAAAGAAGGAACAGTATGCCGGAGAGCAAGGGGGT
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75.1%;
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Pred. No. 7.1e-34;
0; Mismatches 52;
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Pred. No. 8.4e-48;
0; Mismatches 10
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; Patent No. 5182260

APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.

ITILE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
;THOSE INHIBITORS AND COMPOSITIONS USING THEM
;THOMER OF SEQUENCES; 22
;CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,313
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
;FILING DATE: 27-JAN-1989
;FILING DATE: 27-JAN-1989
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US-07-623-611-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Maraganore, John M.

APPLICANT: Chao, Betty H.

APPLICANT: Strauch, Kathryn L.

APPLICANT: Strauch, Kathryn L.

APPLICANT: Thompson, Jeffrey S.

TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND TITLE OF INVENTION: PLATELET ACTIVATION

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 875 Third Avenue - 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 157;
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              STATE: N
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                                                                                                                      APPLICATION NUMBER: UFILING DATE: 19901207 CLASSIFICATION: 435
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5. 5242810
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                                                                                                                                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCTGGCTGTCCCAGAAATCCCTTCCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGTACCGTTTGCCGTCGTGCTCGAGGTGACGACGTTAACGACTACTGCAACGGTATC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCGTCCGGGTGCACAGTGTGCAGAAGGTCTGTGCTGCGACCAGTGCAAATTCATGAAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGAAGAATGCGACTGCGGATCCCCGGGAAAACCCGTGCTGCGACGCGGCCACCTGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGCAGGTTGCCCGCGTAACCCGTTCCA
                                                                                                                                                                                                                                                                                                                              New York
: United States
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                                                                                                                                                                US/07/623,611
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Pred. No. 7.2e-34;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                  TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 bass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application PC/TUS9109108 GENERAL INFORMATION:
                                                                                                                                                                                        ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHOIN DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/US91/09108
FILING DATE: 19911205
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION UMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: C
HYPOTHETICAL: N
ANTI-SENSE: N
                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 715-0600 TELEFAX: (212) 715-0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Biogen, Inc.
TITLE OF INVENTION: *\ ' BIFUNCTIONAL INHIBITORS OF THROMBIN ANDPLATELET ACTIVAT
NUMBER OF SEQUENCES: 14
TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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nes 153; Conserv
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
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F: 875 Third Avenue
New York
                                           NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTTGACCAGTGCAGATTTATGAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
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             linear
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Pred. No. 8.1e-32;
0; Mismatches 58
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                                                     ; ANTI-SENSE: US-07-623-611-10
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US-07-623-611-10
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Patent No.
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Best Local Similarity 72.9
Matches 153; Conservative
Query Match
Best Local
                                                                                                                                                                         TELEFAX: (212) 715-067.
TELEX: 14-3367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,6
FILING DATE: 19901207
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEPHONE: (212) 715-0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strauch, Käthryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN AND
TITLE OF INVENTION: PLATELET ACTIVATION
NUMBER OF SEQUENCES: 14
                                                                                     MOLECULE TYPE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Maraganore, APPLICANT: Chao, Betty
 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue -
CITY: New York
STATE: New York
                                                                                                                                         STRANDEDNESS:
                                                                                                                                                          LENGTH: 288 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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o. 5242810
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56.2%;
72.7%;
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Pred. No. 8.1e-32;
0; Mismatches 58
Score 119.6; DB 1; Pred. No. 1.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29th Floor
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                 Length 288;
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PCT-US91-09108-10
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                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Applicationers in Formation:
                                                                                                                     Matches 152;
                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 3154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-6600
TELEPAX: (212) 715-6674
                                                                                                                                                                                                            MOLECULE TYPE: C
                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Biogen, Inc.
TITLE OF INVENTION: *\ ' BIFUNCTIONAL INHIBITORS OF THROMBIN ANDPLATELET ACTIVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   Local
                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19911205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
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CITY: New Yo
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139 CTGCGTCCGGGTGCTCAGTGCGCTGAAGGTCTGTGCTGCGACCAGTGCAAATTCNNNAAA
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                                                                                                                                   Similarity
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                    CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGGACCAGTGCAGATTTATGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGTACCGTTTGCCCGTCGTGCTCGTGGTGACGACGTTAACGACTACTGCAACGGTATC
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                                                           GGTGAAGAATGCGACTGCGGATCCCCCGGAAAAACCCCGTGCGACGACGCTGCTACCTGCAAA
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875 Third Avenue -
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                                                                                                                   Score 119.6;
Pred. No. 1.1e
0; Mismatches
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; LENGTH: 1851
; TYPE: DNA
; ORGANISM: E.
US-09-608-790-2
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5318899-27
;Patent No.
; LENGTH: 294
5318899-27
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US-09-608-790-2
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                                                                                                                                                                                                    ISRAEL F
                             SEQ ID NO:27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09608790 Patent No. 6413737 GENERAL INFORMATION:
APPLICANT: Cohesion Technologies, APPLICANT: Olsen, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: C99-002
CURRENT APPLICATION NUMBER: US/09/608,790
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/143,128
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wallace, Donald G.
TITLE OF INVENTION: Eccarin Polypeptides, Polynucleotides
                                                                                                       APPLICATION NUMBER: US/
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                  TITLE OF INVENTION: PLATELET NUMBER OF SEQUENCES: 83
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                nt No. 5318899
APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
                                            APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGAAGAATGTGACTGTGGCGCTCCTGC------AAATCCGTGCTGCTGCGATGCTGCA
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Pred. No. 1.8e-28;
0; Mismatches 41
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US-09-026-001A-5
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                                                                                                       Sequence 5, Application US/09026001A Patent No. 6413760
                                                           GENERAL INFORMATION:
APPLICANT: Boodho
APPLICANT: Seehra
 APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MCCARHAGIN,
TITLE OF INVENTION: THERAPBUTIC USES THEREOF
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RESULT 12
5318899-25
5318899-25
;Patent No. 5318899
;Patent Mo. 5318899
;Patent Mo. 5318899
;Patent Mo. 5318899
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TITLE OF INVENTION: PLATELET AGGREGATION
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/48
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
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                                                                   136 AAGGGTACTGTTTGCCGTGTAGCTAAAGGCGACTGGAACGACGATACTTGCACTGGTCAG 195
                                                                                                     121 GAAGGAACAATATGCCGGATGGCAAGGGGTGATGACATGGATGATTACTGCAATGGCATA 180
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196 TCTTGTGACTGCCCGCGTAA 215
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                              TCTGCTGGCTGTCCCAGAAA 200
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Pred. No. 3.9e-24;
0; Mismatches 64
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Pred. No. 3.4e-25
0; Mismatches 6:
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Boodhoo, Amechand Seehra, Jasbir

A COBRA VENOM

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RESULT 14
US-09-026-001A-9
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G11293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                        Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                      APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 13
                                                                                                                                                                             APPLICANT: Boodhoo, Amechand APPLICANT: Seehra, Jasbir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
STREET: 87 Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                        ADDRESSEE:
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                                                                                                                                                                                                                                               , Application US/09026001A 6413760
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                 E: Genetics Institute, Inc
87 CambridgePark Drive
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US-09+026-001A-17
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI52!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2335 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09026001A Patent No. 6413760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: Sako, Dianne
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Releat
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                            TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM TITLE OF INVENTION: THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                    CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                          STREET:
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                                                                                                                                                                                          87 CambridgePark Drive
                                                                                                                                USA
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Pred. No. 1.1e-20;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, SCOTE A.
REGISTRATION NUMBER: 32,724
REGISTRATION UNMBER: G15293B
FELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-026-001A-17
Search completed: December 3, 2004, 20:10:12 Job time : 90 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.8%; Score 89; DB 4; Length 2359; Best Local Similarity 69.7%; Pred. No. 1.1e-20; Matches 154; Conservative 0; Mismatches 55; Indels 12; Gaps
                                                                                                            1525 TGCACTGGCCAATCTGCTGAGTGTCCCACAGACATCTTCCA 1565
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Page 7

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1

Run

9

OM nucleic -

Title: Perfect score:

Scoring table: Sequence:

Minimum DB Maximum DB

BM538117

AGENCOURT MR3-GN022 ha90d11.g BX336226 AU136809

Homo sapi 601283174 BX670023 601302417

RC1-HT025 AU127125 IL5-IT002

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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1: gb
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Gapop 10.0 , Gapext 1.0
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213
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                                                  AA280392
CD535662
BE389727
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BW401492
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                                                BM401624 JILDOFF S
BM401419 GH063F S
BM401444 JHLN04F S
BM401445 JHLN04F S
BM401456 JHLT08F S
BM401457 GH020F S
BM401391 GH010F S
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CF377167 AGENCOURT
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CF377167 AGENCOURT
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AL280392 Zt04h04.r
CD5389922 601282562
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
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BM401624
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ORGANISM
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 409)

Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands the pitviper snake Bothrops insularis through the generation o expressed sequence tags (BSTs)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.

Bothrops insularis (island jararaca)

Bothrops insularis

Bothrops insularis

Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M9911624 409 bp mRNA linear EST 01-MAY-2002
JIID07F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
BM401624
                                                                                                                                                                                                                                                                                                                                                                                                                                            Centro de Biotecnología
Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM401624.1 GI:20376252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12459276
                                                                                                                                                                                                                                                                                                                                                                                                  1: hoplee@usp.br
EST corresponds to cluster
/organism="Bothrops insularis"
/mol type="mRNA"
/db_xref="taxon:8723"
/db_xref="taxon:8723"
/tissue type="venom glands"
/clone_Tib="Snake Bothrops insularis library IL3"
/clone_Tib="Snake Bothrops insularis library IL3"
/clone_Tib="Snake Bothrops insularis pgEM11Zf+; Site_1: Eco
RI, Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Liferechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGBM11Zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paulo Lee Ho
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AF326918
BE390985
BX670023
BX670024
CD361846
CBG000250
BG000250
BM538117
BM336216
BM5316216
AU136809
AW605922
AU1271395
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BG012562
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BQ368056
AA368827
BF987229
C18735
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                                                                                                                                                                                                                                                                                                                                                                                                     BITM08A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA36859 EST80160
BQ368056 QV0-GX014
AA368825 EST80139
BF987229 QV0-GN014
C18735 C18735 Huma
BQ367967 PM4-GN051
BG012562 IL5-GX023
T54209 YA90C07.r2
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AU136809
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Best Local S
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A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centro de Biotecnologia
Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Bothrops.
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Bothrops insularis
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EST.
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399 bp mRNA linear EST 01-GH063F Snake Bothrops insularis library IL2 Bothrops insula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: hoplee@usp.br
EST corresponds to cluster
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/tissue_type="venom glands"
/clone_Tib="Snake Bothrops insularis library II2"
/clone_Tib="Snake Bothrops insularis rought venom glands, Vector: pGEM1IZf+; Site_1: Eco RI; Site_2: Not I; 5ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to CDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM1IZf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paulo Lee Ho
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e-05)."
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/db_xref="taxon:8723"
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91.1%;
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0; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Centro de Biotecnologia
Instituto Butantan
Av. Vital Berazil, 1500, Sao Paulo SP, BRAZIL,
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands
the pitviper snake Bothrops insularis through the generation c
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                              Email: hoplee@usp.br
This EST corresponds to cluster
Seg primer: M13F.
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476 bp mRNA linear EST 01-MAY-20
JH3D12F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
BM401547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12459276
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Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 476)
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/mol_type="mRNA"

/db xref="taxon:8723"

/tisue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/clone_lib="Snake Bothrops insularis site_1: Eco
/note="Organ: venom glands, Vector: pcEmNIZE; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMIZE+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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/mol_type="mRNA"
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ORIGIN
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MEDLINE
PUBMED
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGAGAAGAATGTGACTGTGGCGCTCCTG-----CAAATCCGTGCTGCGATGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centro de Biotecnologia
Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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A survey of gene expression and diversity in the venom glands the pitviper snake Bothrops insularis through the generation expressed sequence tags (BSTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lepidosauria; Squamata; Sclerogle
Viperidae; Crotalinae; Bothrops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bothrops insularis (island jararaca)
Bothrops insularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM401444.1 GI:20376072
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JH1A04F Snake Bc
cDNA 5' similar
BM401444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Paulo Lee Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTGTAAACTGAAATCAGGGTCACAGTGTGGACATGGAGACTGTTGTGAGCAATGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAATGGCATATCTGCTGGCTGTCCCAGAAATCCCTTCCAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTAGCAAATCAGGAACAGAATGCCGGGCATCAATGAGTGAATGTGACCCGGCTGAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCACTGGCCAATCCTCTGAGTGTCCTGCAGATGTCTTCCAT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 444)
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                                 /tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis rought to the program: venom glands; Vector: pGEM112f+; Site_l: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM112f+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hoplee@usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 bp mRNA linear EST 01-MAY-2
Snake Bothrops insularis library IL3 Bothrops insularis
similar to Snake venom metalloproteinase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponds to cluster BITM30A (see Reference)
                                                                                                                                                                                                                                                                                                                                                        /organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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73.0%;
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Pred. No. 2.4e-20;
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JH2B04F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
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Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops insularis

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viperidae; Crotalinae; Bothrops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This EST corresponds to cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Paulo Lee Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTGTTGTGACCAGTGCAGATTTATGAAAGAAGGAACAATATGCCGGATGGCAAGGGGT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGTGTTGTGACCAGTGCAGATTTAAGGGAGCAGCATCAGAATGCCCGGTCAGCAAGGAGT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATCCGTGCTGTGATGCTGCAACCTGTAAACTACAGTCATGGGTAGAGTGTGAATCTGGA 89
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/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11Zf+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dr) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGRM11Zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
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                                                                                                                                                                                                                                                                                                                                                   /organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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75.8%;
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Pred. No. 4.2e-20)
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BM401556
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Best Local Sim:
Matches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ACCTGTAAACTACACTCATGGGTAGAGTGTGAATCTGGAGAGTGTTGTGACCAGTGCAGA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ACCTGTAAACTGAGACCAGGGGGGGGAGTGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGA 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands
the pitviper snake Bothrops insularis through the generation c
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centro de Biotecnologia
Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hoples@usp.br
This EST corresponds to cluster
Seq primer: M13F.
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Bothrops insularis
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JH3F08F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM401556.1 GI:20376184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TECACTECCAATCTCCTGAGTGTCCCATAGATGACTTCAA 276
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                                         /organism="Bothrops insularis"
//organism="Bothrops insularis"
//db_xref="taxon:8723"
//db_xref="taxon:8723"
//tissue_type="venom glands"
//clone_Tib="Snake_Bothrops insularis_library_II3"
//clone_Tib="Snake_Bothrops insularis_library_II3"
//clone_Tib="Snake_Bothrops insularis_libraty_II3"
//clone_Tib="Snake_Ti
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Pred. No. 4.6e-20;
0; Mismatches 48
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Query Match

Score 100.2;

DB 4;

Length 432

Query Match Best Local Similarity

46.1%; 72.6%;

Score 98.2; DB 4; Pred. No. 2e-19;

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REFERENCE
AUTHORS
TITLE
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BM401456
ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 TTTATGAAAGAAGGAACAATATGCCGGATGGCAAGGGGGTGA---TGACATGGATGATTAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 ACCTGTAAACTACACTCATGGGTAGAGTGTGAATCTGGAGAGTGTTGTGACCAGTGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hoplee@usp.br
This EST corresponds to cluster
Seq primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Centro de Biotecnología
Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands the pitviper snake Bothrops insularis through the generation cappressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 377)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Paulo Lee Ho
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                                  /tissue_type="venom glands"
/clone_Tib="Shake Bothrops insularis library IL3"
/clone_Tib="Shake Bothrops insularis rorgan: venom glands; Vector: pGEM11Zf+; Site_1: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to CDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The CDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGBM11Zf+ vector (promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insularis
                                                                                                                                                                                                                                                                                                                                       /organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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0; Mismatches 48
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48;

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4 GAAGAATGTGACTGTGGCGCTCCTG------CAAATCCGTGCTGCGATGCTGCAACC

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REFERENCE
AUTHORS
TITLE
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MEDLINE
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Query Match
Best Local Similarity
Matches 108; Conserv
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Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
22347338
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Bothrops insularis
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EST.
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420 bp mRNA linear EST 01-MAY-2
JL2E03F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepidosauria; Squamata; Sclerogle
Viperidae; Crotalinae; Bothrops
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Paulo Lee Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGAATGTGACTGTGGCACTCCTGAAAATTGTCAAAATGAGTGCTGCGATGCTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGCCAATCCTCTGAGTGTCCTGCAGATGTCTTCCAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGGCATATCTGCTGGCTGTCCCAGAAATCCCTTCCAT 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: hoplee@usp.br
EST corresponds to cluster BITM16A (see Reference)
                                                                                        /organism="Bothrops insularis"
//mol_type="mRNA" 8723"
//db xref="taxon:8723"
//tissue_type="venom glands"
//clone_Tib="Snake Bothrops insularis library IL3"
//clone_Tib="Snake Bothrops insularis library IL3"
//clone_Tib="Snake Bothrops insularis library insularis stee_2: Not I, 500 of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA synthesis and Cloning (LifeTechnologise). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGRNI2f+ vector (Fromega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                  35.0%;
Score 74.6; DB
Pred. No. 4.3e-1
0; Mismatches
                                     DB 4;
                                   Length 420;
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  Gaps
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                                                                                                                   Query Match
Best Local (
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                                                                                                  107;
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                                                        61 CTGAGACCAGGGGGGGAGTGTGCAGAAGGACTGTGTTGTGACCAGTGCAGATTTATGAAA 120
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                                                                                                                     Similarity
                       CTGAAATCAGGGTCACAGTGTGGACATGGAGACTGTTGTGAGCAATGCAAATTTAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hoplee@usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .411
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                                                                                                                   32.0%;
                                                                                                                   Score 68.2; DB 4;
Pred. No. 4.2e-10;
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                                                                                                    Mismatches
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128
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Bothrops Insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Serpentes; Colubroidea;
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Centro de Biotecnología
Centro de Biotecnología
Centro de Biotecnología
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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1 (bases 1 to 411)

Junqueira-de-Azevdo,I.L.M. and Ho,P.L.

Junqueira-de-Azevdo,I.L.M. and diversity in the venom glands A survey of gene expression and diversity in the venom glands the pitviper snake Bothrops insularis through the generation cexpressed sequence tags (ESTs)

expressed sequence tags (ESTs)

Gene 29 (1-2), 279-291 (2002)
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/organism="Bothrops insularis"
/mol_type="mgRNA"
/db_xref="taxon:8723"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_Tib="Snake_Bothrops insularis_library_IL2"
/clone_Tib="Snake_Bothrop
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s insularis cDNA
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BM401391
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Instituto Butantan
Av. Vital Barazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Bothrops insularis
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                                                                                                                                                                              CTGAGACCAGGGGCGCAGTGTGCAGAAGGACTGTGTTGTTGTGAACCAGTTGCAGATTTATGAAA 120
       ATATCTGCTGGCTGTCCCAGAAATCCCTTCCAT
                                                                                                 GAAGGAACAATATGCCGGATGGCAAGGGGTGA---TGACATGGATGATTACTGCAATGGC 177
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/clone Tib="snake Bothrops insularis library IL2"
/clone Tib="snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEMILZf+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMILZf+ vector (promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
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/mol_type="mRNA"
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Tel: 55 11 37 26 7222 e
Fax: 55 11 37 26 1505
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GH020F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom metalloproteinase, mRNA sequence.

BM401397
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Centro de Biotecnologia
Instituto Butantan
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1 (bases 1 to 527)
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s EST corresponds to cluster
primer: M13F.
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/db_xref="taxon:8723"

/tissue type="venom glands"

/clone_Tib="Snake Bothrops insularis library IL2"

/clone_Tib="Snake Bothrops insularis pgEM12f; Site_1: Eco

/note="Organ: venom glands; Vector: pgEM12f; Site_1: Eco

/note="Organ: venom glands; Vector: pgEM12f; Site_1: Site_2: Not 1; Sug of mRNA from Bothrops insularis

venom glands were primed with oligo-(dT) and reverse

venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in

agarose gel electrophoresis, linked to Eco RI adapters and

directionally cloned in pgEM12f+ vector (Promega). ESTs

were generated from random clones and grouped in unique

sequences. The putative identification of each EST or

cluster was obtained through Blast searches (e-value <
e-05)."
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Pred. No. 4.5e-10;
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Length 527; Indels

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by MRNA linear EST 01-GH016F Snake Bothrops insularis library IL2 Bothrops insula 5' similar to Snake venom metalloproteinase, mRNA sequence. BM401393
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Av. Vital Brazil, 1500, Sao Pau
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hople@usp.br
This EST corresponds to cluster
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                                                                                                                                                                                                                                                                       CAATCCTCTGAGTGTCCTGCAGATGTCTTCCAT
                                                                                                                                                                                                                                                                                                                         ATATCTGCTGGCTGTCCCAGAAATCCCTTCCAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGAACAATATGCCGGATGGCAAGGGGTGA---TGACATGGATGATTACTGCAATGGC 177
                                                                                                                                                                                                                                                                                                                                                                                               TCAGGAACAGAATGCCGGGCATCAATGAGTGAATGTGACCCGGCTGAACACTGCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAATCAGGGTCACAGTGTGGACATGGAGCACTGTTGTGAGCAATGCAAATTTAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="venom glands"
/clone Tib="Snake Bothrops insularis library IL2"
/clone Tib="Snake Bothrops insularis pgEM11Zf+; Site_1: Eco
/note="Organ: venom glands; Vector: pgEM11Zf+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11Zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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/db_xref="taxon:8723"
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Pred. No. 4.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                    153
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                                                                                                      EST 01-MAY-2002
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                                                                      insularis cDNA
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AUTHORS
TITLE
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CF377167
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MEDLINE
PUBMED
                                   ORGANISM
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VERSION
KEYWORDS
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                       121 CAATCCTCTGAGTGTCCTGCAGATGTCTTCCAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAAGGAACAATATGCCGGATGGCAAGGGGTGA---TGACATGGATGATTACTGCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCAGGAACAGAATGCCGGGCATCAATGAGTGAATGTGACCCGGCTGAACACTGCACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hoplee@usp.br
This EST corresponds to cluster
Seq primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Centro de Biotecnología
Instituto Butantan
Av. Vital Barazil, 1500, Sac
Tel: 55 11 37 26 7222 ext.
Fax: 55 11 37 26 1505
                                                                                                                                                     GF377167

AGENCOURT 15341148 NICHD XGC Swbin IMAGE:7004048 5', mRNA sequence.
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae, Crotalinae; Bothrops.
1 (bases 1 to 565)
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Bothrops insularis
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EST.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                   CF377167
CF377167.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAAATCAGGGTCACAGTGTGGACATGGAGACTGTTGTGAGCAATGCAAATTTAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="venom glands"
/clone_lib="snake Bothrops insularis library IL2"
/clone_lib="Snake Bothrops insularis library IL2"
/clone_lib="Snake Bothrops insularis program venom glands, vector: pGEMIIZE+; Site_l: Eco RI; Site_l: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(GT) and reverse transcribed to CDNA using Superscript plasmid System for CDNA Synthesis and Cloning (Liferechnologies). The CDNAS were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11ZF+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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/mol_type="mRNA"
/db_xref="taxon:8723"
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                                                                                                      GI:34314611
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Pred. No. 4.5e-10;
0; Mismatches 43
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is cDNA clone
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AI525705
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Best Local S
Matches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-c@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14700 row: m column: 06
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PT1.3.04 H03.r tumor1 Homo
AI525705
AI525705.1 GI:4439840
EST.
  Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 845)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 61.5
15; Conservative
                                                                                                                                                                                                                                                   CCGGGTC
                                                                                                                                                                                                                                                                                        CCATGCC 213
                                                                                                                                                                                                                                                                                                                                                                 TGA---TGACATGGATGATTACTGCAATGGCATATCTGCTGCTGCTGTCCCAGAAATCCCCTT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGTGTGTGACCAGTGCAGATTTATGAAAGGAAGGAACAATATGCCCGGATGGCAAGGGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATCCATGTTGCGATGCTGCCACCTGCAAAAAGAAGCCAAATGTTCAATGTACAGGGGG 424
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                                                                                                                                                                                                                                                                                                                                  AGAATGCTGTGATAACTGTATGATCAAGGCAGCCGGACATGTATGCAGAGCTAGTAAGGG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone Tib="NICHD XGC_Swb1N"
/notes "Vector: pExpress-1; Site 1: EcoRV; Site 2: Not1;
/notes "Vector: pExpress-1; Site 1: EcoRV; Site 2: Not1;
Bulk tissue was collected from a whole 10 month old male
from the P6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD_XGC_Swb1). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
                                                                                                                                                                                                                                                   551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:7004048"
/tissue_type="whole_body"
/clone_lib="NICHD_XGC_Swb1N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus tropicalis"
/mol_type="mRNA"
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Metazoa; Chordata; Craniata;
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                                                                                                                                          gd 638
                                                                                                                      sapiens
                                                                                                                        mRNA
cDNA
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П,
  Vertebrata; Euteleostomi
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REFERENCE
AUTHORS
Search completed: December Job time: 2977 secs
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Best Local Similarity
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                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                      7 GAATGTGACTGTGGGGCTCCTGCAAATCCGTGCGTGCGATGCTGCAACCTGTAAACTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington
Department of Molecular Biotechnology, Box 357730, University of
Washington, Seattle, WA 98195
Tel: 5105280100
Fax: 5105280108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 863)

Huang,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer expression profiling by cDNA sequencing analysis Genomics 59 (2), 178-186 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: huanggm@yahoo.com.
Location/Qualifiers
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                                                                               CATCATGCCCAGAAAACCACT
                                                                                                                  CTGGCTGTCCCAGAAATCCCT 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="tumor1"
/note="0rgan; Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."
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                 3, 2004, 20:08:33
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Listing first 45 summaries
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Perfect score:
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2: pir2:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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3, 2004, 21:14:23; Search time 51 Seconds (without alignments) 137.722 Million cell upda
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nemorrhagic prote: fertilin beta - c:		atrolysin A (EC	metalloproteinase	platelet aggregat		jararhagin C precu	halysase - Gloydiu	coagulation factor	vascular apoptosi	bitistatin - puff	ecarin precursor	bitan alpha - puf	cytotoxic factor	atrolysin E (EC 3

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platelet-aggregation disintegrin (brevicaudin) (Species: Gloydius halys brevicaudus C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2012 #sequence_revision 0
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A;Accession: A59410
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-73 <TER>
A;Cross references: UNIPROT: C90220
C;Keywords: anticoagulant; integrin inhibitor; venom
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Fukuoka Univ. Sci. Reports 30, 71-78, 2000 Fukuoka Univ. Sci. Reports 30, 71-78, 2000 A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd
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A;Molecule type: prottein
A;Residues: 1-71 <TER>
A;Cross-references: UNIPROT:Q90WC0
C;Keywords: anticoagulant; integrin inhibitor; venom
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A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloyd
A;Reference number: A59409
A;Accession: A59409
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Score 400; DB 2;
Pred. No. 2.3e-31;
2; Mismatches 3
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applaggin - eastern cottonmouth
C:Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33990
R:Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marzec, U.M.; Harker, Proc. Natl. Acad. Sci. U.S.A. 86, 8050-8054, 1989
A;Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a p A;Reference number: A33990; MUID:90046735; PMID:2510158
A;Accession: A33990
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 cCHA>
A;Cross-references: UNIPROT:P16338
C;Superfamily: unassigned disintegrins; disintegrin homology
F;1-68/Domain: disintegrin homology (fragment) <DIS>
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A;Accession: A59411
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 <TER>
A;Cross-references: UNIPROT:Q90220
C;Keywords: anticoagulant; integrin inhibitor; venom
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C;Species: Gloydius halys brevicaudus
C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2002
C;Accession: A59411
R;Teradd, S.
Fukuoka Univ. Sci. Reports 30, 71-78, 2000
albolabrin
C;Species:
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                                                                                                     GISAGCPRNPFH
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4; Mismatches 2
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C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_cha C;Accession: 335982 (C;Accession: 335982; M:J.; Pitti, R.M.; Lipari, M.T.; Nar Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990 A;Title: Platelet glycoprotein IIb-IIIa protein antagonists A;Reference number: A35982; MUID:90207217; PMID:2320569
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R;Jaseja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer
Bur. J. Biochem. 218, 853-860, 1993
A;Title: (1)H-NMR studies and secondary structure of the A;Reference number: S43021; MUID:94109384; PMID:9281937
A;Accession: S43021
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F;1-69/Domain: disintegrin homology (fragment)
F;51-53/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-73 <DEN>
A;Cross-references: UNIPROT: P17496
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A;Accession: E35982
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C;Species: Trimeresurus gramineus (Indian green tree viper)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
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A;Molecule type: protein
A;Residues: 1-73 <JAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: inhibits cell adhesion and platelet aggregation C;Superfamily: unassigned disintegrins; disintegrin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Funct:
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Best Local
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                                                               61 GISAGCPRNPFHA 73
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Pred. No. 1.6e-30;
Pred. No. 5;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                Mismatches
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1.6e-30;
hes 5;
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A;Molecule type: protein
A;Rosidues: 408-419 <HU2>
C;Superfamily: trigramin precursor; disintegrin homology
C;Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc;
F;1-18;Domain: signal sequence #status predicted <SIG>
F;198-476/Domain: disintegrin homology <DIS>
F;408-479/Product: trigramin #status experimental <MAT>
F;408-479/Product: crigramin #status experimental <MAT>
F;408-479/Product: crigramin #status predicted
F;333,337,343/Binding site: zinc (His) #status predicted
F;333,337,343/Binding site: zinc (His) #status predicted
F;334/Active site: Glu #status predicted
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A;Residues: 408-479 <hUA>
A;Residues: 408-479 <hUA>
A;Residues: TF; Holt, J.C.; Lukasiewicz, H.; Niewiarowski,
J. Biol. Chem. 262, 16157-16163, 1987
J. Biol. Chem. 262, 16157-16163, 1987
A;Title: Trigramin. A low molecular weight peptide inhibit
A;Reference number: A29784; MUID:88058981; PMID:3680247
A;Recession: A29784
                                         A;Molecule type: protein
A;Residues: 206-214;221-233;299-308;310-344;451-453;460-484 <CH2>
C;Comment: This protein, a new metalloproteinase-disintegrin protein,
                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-494 <CHE>
A;CREsidues: GB:AY364231
A;Cross-references: GB:AY364231
A;Experimental source: Crude venom
A;Accession: PC7231
                                                                                                                                                                                                                                                                                           R;Chen, R.Q.; Jin, Y.; Wu, J.B.; Zhou, X.D.; Lu, Q.M.; Wang, W.Y.; Xiong, Y.L. Biochem. Biophys. Res. Commun. 310, 182-187, 2003
A;Title: A new protein structure of P-II class snake venom metalloproteinases: It A;Reference number: JC8020; PMID: 14511668
A;Accession: JC8020; PMID: 14511668
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A;Title: Trigramin: primary structure and its inhibition of von Willebrand factor bindin A;Reference number: A30065; MUID:89229063; PMID:2653425
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N;Contains: hemorrhagic proteinase (EC 3.4.24.-); platelet aggregation inhibitor

C;Species: Trimeresurus gramineus (Indian green tree viper)

C;Date: 16-Sep_1992 #sequence revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: S12589; A30065; A29784

R;Neeper, M.P.; Jacobson, M.A.
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A; Title: Sequence of a cDNA encod
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Best Local S
Matches 62
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                                   This protein, ICSO of 120nM.
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Jerdonitin; metalloproteinase-disintegrin; platelet aggregation;
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62; Conserv
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Pred. No. 1.9e-29;
7; Mismatches 4
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A;Cross-referen
C;Superfamily:
F;3-69/Domain:
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A;Accession: C35982
A;Molecule type: protein
A;Residues: 1-72 <DE2>
C;Superfamily: disintegrin homolog
C;Keywords: venom
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CySpecies: Trimeresurus gramineus (Indian green tree viper)
CyBate: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
CyAccession: D35982; C35982
RyDennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A;Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: A;Reference number: A35982; MUID:90207217; PMID:2320569
                                                                                                                                                                                                                                                                                platelet aggregation disintegrin (cer
C;Species: Crotalus viridis cerberus
C;Date: 12-Mar-1993 #sequence_revisio
C;Accession: B43020
                                                                                                                                                                                                         R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillig
J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities
A;Reference number: A43019; MUID:93123215; PMID:8419314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-73 < DEN>
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                                                                                                                                                                                     A; Accession: B43020
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Best Local S
Matches 63
Query Match
Best Local S
Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GISAGCPRNPFHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
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h 82.2%;
Similarity 83.3%;
60; Conservative
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                                                                        unassigned o
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                                                                                                            UNIPROT: P31985
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                                                                                              disintegrins;
                                                                          homology
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Score 356; DB 2;
Pred. No. 3.4e-27;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                        (cereberin), venom - Arizona bl
erus (Arizona black rattlesnake)
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Pred. No. 3.3e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 379; DB 2;
Pred. No. 2.3e-29;
5; Mismatches 6;
                                                                            <DIS>
                                                                                                                                                                                                                                                                                                      12-Mar-1993 #text_change
                                                                                            disintegrin homology
                                                                                                                                                                                                                                                                  M.A.; Phillips,
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                                    Length 72;
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H
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                                                                                                                                                                                                                                disintegrins
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60;

Indels

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Gaps

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platelet aggregation disintegrin (lachesin), venom - bushmaster C.Species: Lachesis muta (bushmaster)
C.Species: Lachesis muta (bushmaster)
C.Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C.Accession: E43019
R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; P.
J. Biol. Chem. 268, 1058-1065, 1993
A.;Title: Characterization of the integrin specificities of disintegrins isolated A; Reference number: A43019; MUID:93123215; PMID:8419314
A.;Recession: E43019
A.;Status: preliminary
A.;Cross-references: UNIPROT:P31990
C.;Superfamily: disintegrin homology
F;3-69/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet aggregation disintegrin (basilicin), venom - Mexican West-Coast rattlesnake C.Species: Crotalus basiliscus basiliscus (Mexican West-Coast rattlesnake) C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004* C;Accession: 143019
C;Accession: 143019
R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 193
A;Title: Characterization of the integrin specificities of disintegrins isolated from An A;Accession: 143019; MUID:93123215; PMID:8419314
A;Accession: 143019
A;Status: preliminary A;Molecule type: protein A;Aresidues: 1-72 <SCA>
A;Cross-references: UNIPROT:P31981
C;Superfamily: disintegrin homology <DIS>
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RESULT
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Best Local S
Matches 59
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Best Local S
Matches 60
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                                                                                                                                                                                                                                        Similarity
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                                                             GOSADCPRNGYY 72
                                                                                               GISAGCPRNPFH
                                                                                                                                     EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCT
                                                                                                                                                                             EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 60
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                                                                                                                                                                                                                 Score 350; DB
Pred. No. 1.3e
5; Mismatches
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Pred. No. 4.2e-27;
4; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten,
                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                       Length 73
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R,Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfster J. Biol. Chem. 268, 1058-1065, 1993
A,Title: Characterization of the integrin specificities of disintegrins isolated from A,Reference number: A43019, MUID:93123215; PMID:8419314
A,Accession: G43019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Scarborough, R.M.; Rose, J.W.; Hsu, M.A.; Phillips, D.R.; Fried, V.A.; Campbell, A.M. J. Biol. Chem. 266, 9359-9362, 1991
A;Title: Barbourin. A GPIIb-IIIa-specific integrin antagonist from the venom of Sistrur A;Reference number: A40003; MUID:91236695; PMID:2033037
A;Accession: B40003
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B40003
platelet aggregațion disintegrin (jararacin), venom - jararacussu
C;Species: Bothrops jararacussu (jararacussu)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 10-Jul-1998
C;Accession: A43020
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C;Superfamily: unassigned disintegrins, disintegrin homology
F;3-69/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          platelet aggregation disintegrin (tergeminin), venom - western massasauga C;Species: Sistrurus catenatus tergeminus (western massasauga) C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004 C;Accession: B40003
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A;Molecule type: protein
A;Residues: 1-71 <SCA>
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C;Species: Crotallus viridis viridis (prairie rattlesnake)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C;Accession: G43019
                                                                              A43020
                                                                                                 RESULT 15
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A;Residues: 1-73 <SCA>
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSADCPRINEFH
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                                                                                                                                                           GOSADCPRN
                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 2.4e-26;
5; Mismatches 6;
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Pred. No. 1.9e-26;
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R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Ar J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated A;Reference number: A43019; MUID:93123215; PMID:8419314
A;Accession: A43020

from

preliminary

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A;Molecule type: protein
A;Residues: 1-73 <SCA>
C.Superfamily: unassigned disintegrins; disintegrin homology
C.Superfamily: unassigned momology <DIS>

Query Match
Best Local Similarity 80.8%; Pred. No. 4.6e-26;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
Matches 59; Conservative 1; Mismatches 13; Indels 2; Indels 0;
Matches 59; Conservative 1; Mismatches 13; Indels 2; Indels 0;
Matches 13; Indels 2; Indels 2; Indels 2; Indels 2; Indels 2;
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Result No.
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Perfect
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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433
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(c) 1993 - 2004 Compugen Ltd
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US-09-776-268A-1
US-09-460-295B-1
US-09-460-295B-1
US-09-460-295B-1
US-09-460-295B-1
US-09-963-674-14
US-08-993-145-15
US-09-243-640-13
US-09-243-640-13
US-09-243-640-15
US-09-23-14-15
US-09-23-611-8
US-09-23-611-8
US-07-623-611-8
US-07-623-611-9
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5182260-2
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                Sequence 1, Appli Sequence 7, Appli Sequence 10, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Ap
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Patent No. 5182260
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## ALIGNMENTS

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PATERIT NO. 5182260

PATERIT NO. 5182260

APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A. APPLICATI. INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING; INHIBITORS AND COMPOSITIONS USING THEM NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/430,313

FILING DATE: 01-NOV-1989

PRIOR APPLICATION NUMBER: 303,585

FILING DATE: 27-JAN-1989

; SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DAN SEQUENCES ENCODING SNAKE VENOM
INTELS OF INVENTION: DAN SEQUENCES ENCODING SNAKE VENOM
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
INHIBITORS AND COMPOSITIONS USING THEM
INTELS OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,313
FILING DATE: 01-NOV-1989
PRIOR APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
FILING DATE: 27-JAN-1989
SEQ ID NO:21:
                                                                                                                                                                                                                                                                       RESULT 2
5182260-2
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5182260-21
;Patent No. 5182260
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Best Local S
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Similarity 90.3%;
65; Conservative
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Pred. No. 1.6e-30;
5; Mismatches 2;
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Gaps

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RESULT 4
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5182260-2
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; ORGANISM: Agkistrodon halys brevicaudus
US-09-776-268A-1
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                                                                                                                                                                                                                  Patent No. 5380646
GENERAL INFORMATION:
APPLICANT: Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: KR 98-23778
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                       Sequence 10, Application US/07965674 Patent No. 5380646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09776268A Patent No. 6537551
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHUNG, Kwang Hoe
APPLICANT: KANG, IN-Chaol
TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
FILE REFERENCE: 0136/1F733-US1
CURRENT APPLICATION NUMBER: US/09/776,268A
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: US 09/335,088
PRIOR APPLICATION NUMBER: US 09/335,088
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR FILING DATE: 1999-06-17
PRIOR PRIOR PRIOR DATE: 1999-06-17
PRIOR PRIOR PRIOR DATE: 1999-06-19
                                                                                                                                        APPLICANT: Knight, Linda C.
TITLE OF INVENTION: Thrombus Detection Using
TITLE OF INVENTION: Radiolabelled Disintegrins
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                       ADDRESSEE: Temple University - Of The Common ADDRESSEE: wealth System of Higher Education
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                                                                    ?: 406 University Services Building
Philadelphia
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                                                    Pennsylvania
                                   U.S.A.
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Pred. No. 7.1e-30;
2; Mismatches 5;
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                                                                                                                                   Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS'
TITLE OF INVENTION: OTHER CONDITIONS
TITLE REFERENCE: 1279-338C3/09801388
CURRENT APPLICATION NUMBER: US/09/460,295B
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09460295B Patent No. 6710030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: NO. 5380646e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/Z
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                61
60 GISAGCPRNPFH
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                                                                                                                                   Similarity 90.3
65; Conservative
                                                                                                                                                                                                                                                                                        PatentIn version 3.1
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                    GISAGCPRNPFH 72
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                                                             EAGEECDCGSPENFCCDAATCXLRPGAQCAEGLCCDQCKFWKEGTVCR-ARGDDVNDYCN
                                                                                                EAGEECDCGAPANECCDAATCKLREGAQCAEGLCCDQCREMKEGTICKMARGDDMDDYCN 60
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71
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                                                                                                                                 Score 392.5; DB 4
Pred. No. 1.2e-29;
5; Mismatches 1
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Pred. No. 1.2e-29;
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                                                                                                                                                                  DB 4;
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                                                                                                                                                                  Length 71;
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US-07-965-674-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: None
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Applicat GENERAL INFORMATION:
                                                                                                                                                          Sequence 14, Application US/07965674
Patent No. 5380646
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MG-DOS
SOFTWARE: WOrdPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 965,674
FILING DATE: 19 October 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Temple University - Of The APPLICANT: System of Higher Education APPLICANT: Knight, Linda C. and APPLICANT: Maurer, Alan H.
                                                                     APPLICANT: Knight, Linda C.
TITLE OF INVENTION: Thrombus
TITLE OF INVENTION: Radiolal
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION:
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ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                  61 GISAGCPRNPFH 72
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65; Conservative
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                                                                                                          Thrombus Detection Using Radiolabelled Disintegrins
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Pred. No. 1.2e-29;
5; Mismatches 1;
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61 GISAGCPRNPFHA 73

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                                                                                                         , OTHER INFORMATION: Description of Artificial Sequence: No. US-08-993-165-15
                                                                                                                                                                                    APPLICANT: Ungr. Evan C
APPLICANT: Wu, Yungiu
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOCTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: DEF
                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Applica Patent No. 6123923 GENERAL INFORMATION:
                                        Matches
                                                                      Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MONACO, Daniel A.
REGISTRATION NUVMER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19921019
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                          FEATURE:
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SOFTWARE: WORDPEFFECT 5.1
CURRENT APPLICATION NUMBER: US/07,
APPLICATION NUMBER: US/07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett COMPUTER: IBM PS/2
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                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
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1 EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
                                                        Similarity
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                                        Conservative
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                                                        90.3%;
87.7%;
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                                                        Score 391; DB 3;
Pred. No. 1.6e-29;
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                                         Mismatches
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                                                                     Length 73;
                                        Indels
                                                                                                                             6123923el Sequence
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; TYPE: PRT
; CRCANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely
US-08-929-847-15
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 13
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR AFFLICATION NUMBER: 09/218
PRIOR AFFLICATION NUMBER: 09/218
PRIOR FILING DATE: 1998-12-22
PRIOR AFFLICATION NUMBER: 60/07:
PRIOR AFFLICATION NUMBER: 60/07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: DUP-0463
CURRENT APPLICATION NUMBER: US/09/243,640
CURRENT FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 08/660,032
PRIOR FILING DATE: 1996-06-06
PRIOR PPLICATION NUMBER: 08/640,464
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR APPLICATION NUMBER: 08/497,684
                                                                                                                                                                     APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
FILE REFERENCE: BMS0441

CURRENT APPLICATION NUMBER: US/08/929,847

CURRENT FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15

LENGTH: 73
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APPLICANT: Shen, Dekang
APPLICANT: Wu, Guanli
TITLE OF INVENTION: NO
TITLE OF INVENTION: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, App. No. 652121
 Matches 64;
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/08929847 Patent No. 6548047
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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 Similarity 87. 64; Conservative
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PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GISAGCPRNPLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAGEDCDCGSPANFCCDAATCKLLFGAQCGEGLCCDQCSFMKKGTTCRRARGDDLDDYCN 60
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Shen, Dekang
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                                                                                           Completely synthetic sequence
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                   90.3%;
87.7%;
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   4; Mismatches
                   Score 391;
Pred. No. 1
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Pred. No. 1.6e-29;
4; Mismatches 5
                   DB 4;
L.6e-29;
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                                   Length
 Indels
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Gaps
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Sequence 9, Application US/09460295B
PATENT NO. 6710030
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND ME
FILE REFERENCE: 1279-338C3/09801388
CURRENT APPLICATION NUMBER: US/09/460,295B
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US/09/460,295B
CURRENT FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
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                                                                                                                 ; OTHER INFORMATION: Completely synthetic sequence US-09-813-484-15
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US-09-460-295B-9
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                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/929,847
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseo
TITLE OF INVENTION: Filled Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09813484 Patent No. 6716412
                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-813-484-15
                                                                                                                                                                                                                                                                                                     FILE REFERENCE: UNGR1600
CURRENT APPLICATION NUMBER: US/09/813,484
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Trimeresurus albolabris
                                                                                                                                                       FEATURE:
                                                                                                                                                                                                       ENGTH: 73
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                                                                     Similarity
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EAGEECDCGAPANFCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
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                                                     Conservative
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                                                                     90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%;
                                                   Score 391; DB
Pred. No. 1.6e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 391; DB 4;
Pred. No. 1.6e-29;
4; Mismatches 5
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                                                                   DB 4;
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                                                                                 Length 73
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PCT-US93-09523-14
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US-07-623-611-5
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Best Local S
Matches 64
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GENERAL INFORMATION:
APPLICANT: Temple University - Of The Commonwee
APPLICANT: System of Higher Education
APPLICANT: Knight, Linda C. and
APPLICANT: Maurer, Alan H.
TITLE OF INVENTION: Thrombus Detection Using
TITLE OF INVENTION: Radiolabelled Disintegrins
                                                                                          Sequence 5, Application US/07623611
Patent No. 5242810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
GENERAL INFORMATION:
APPLICANT: Maragai
APPLICANT: Chao, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-173 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 965,674
FILING DATE: 19 October 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/09523
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Similarity 87.7%;
64; Conservative '
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Maraganore, John M. Chao, Betty H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (215) 568-5549
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Sequence 8, App.
Sequence 9, Sequence 9, Sequence 9, App.
Sequence 9, Sequence 9, App.
Sequence 8, App.
Sequence 9, App.
Sequence 9
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CITY: New York STATE: New York COUNTRY:

United States

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MOLECULE TYPE: protein US-07-623-611-5
RESULT 15
                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION UNMBER: 27,794
REFERENCE/DOCKET NUMBER: B154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-6600
TELEFAX: (212) 715-0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strauch, Kathryn L.
APPLICANT: Thompson, Jeffrey S.
TITLE OF INVENTION: BIFUNCTIONAL INHIBITORS OF THROMBIN ITITLE OF INVENTION: PLATELET ACTIVATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UPFILING DATE: 19901207 CLASSIFICATION: 435
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                                                                                                                        64;
                                                      88 GISAGCPRNPFH 99
                                                                                    61 GISAGCPRNPFH 72
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: United States
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                       linear
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Pred. No. 2.7e-29;
5; Mismatches 3
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                                                                                                                                                                                                                               Length 99;
                                                                                                                                                                                               Indels
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SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,611
FILING DATE: 19901207

CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 8154
TELEOPONE: (212) 715-0674
TELEX: 14-8367 IN NO. 8:
SEQUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Result
No.
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    December 3, 2004, 21:38:18 ; Search time 104 Seconds
(without alignments)
250.322 Million cell updates/sec
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433
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Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USOA_PUBCOMB.pep:*
                                                                                                                                                                                                                                                           Length
   73
71
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US-09-776-268A-1
US-09-832-501-37
VUS-10-439-532-7
US-10-439-532-7
US-10-439-532-9
US-10-112-584-9
US-10-112-584-9
US-10-046-801-15
US-10-0439-532-8
US-10-439-532-2
US-10-0712-584-8
US-10-112-584-8
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                                                                                                                                                                                                                                                                                                                SUMMARIES
Sequence 1, Appli
Sequence 37, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 15, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 15, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
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Sequence 2, Appli
                                                                                                                                                                                                                                                             Description
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US-09-776-268A-1
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                                                                                                                                  Query Match
Best Local S
Matches 66
61 GISAGCPRNPFHA 73
                                                                                                                                    66;
                                                                                                                                                      Similarity
                                                                                                                                    Conservative
                                                                                                                                                      91.2%;
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## ALIGNMENTS

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Sequence 1, Application US/0977626BA
Publication No. US20010023242A1

GENERAL INFORMATION:
APPLICANT: KIM, Doo-Sik
APPLICANT: KIM, Doo-Sik
APPLICANT: KIM, Doo-Sik
APPLICANT: KANG, In-Cheol
ITITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
FILE REFERENCE: 0136/1F733-US1
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: US/09/776,268A
CURRENT FILING DATE: 2902-06-17
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: KR 98-23778
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTING DATE: 1998-06-23
INGRANISM: Agkistrodon halys brevicaudus
US-09-776-268A-1
                            1 EAGESCDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
EAGEECDCGSPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRATRDDLDDYCN
                                                                                                  Score 395; DB 9; Length 73; 
pred. No. 3.5e-31; 
2; Mismatches 5; Indels
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GISAGCPRNPFHA 73

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; ORGANISM: Agkistrodon piscivorus
US-09-832-501-37
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FILE REFERENCE: PFS42
CURRENT APPLICATION NUMBER: US/09/832,501
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10439532
Publication No. US20030186884A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: CONFORTROSTATIN STRICK STR
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 71
TYPE: PRT
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Best Local
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APPLICANT: Ballance,
APPLICANT: Sleep, D
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SEQ ID NO 37
LENGTH: 71
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                                                                                                                                                                                             Similarity
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65; Conservative
                                                        EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 60
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EAGEECDCGSPENPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCR-ARGDDVNDYCN 59
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Sadeghi, Homa
Prior, Christopher P.
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                                                                                                                                                     Conservative
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                                                                                                                                             Score 392.5; DB 14;
Pred. No. 6e-31;
5; Mismatches 1;
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APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: MATAIAND, FRANCIS S.
APPLICANT: MATAIAND, FRANCIS S.
APPLICANT: MATAIAND, FRANCIS S.
APPLICANT: MATAIAND, MATHDOS FOR ITS USE IN PREVENTING METAS
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS
FILE REFERENCE; 1279-338N3/0801388
FILE REFERENCE; 1279-338N3/0801388
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-60-08
PRIOR APPLICATION NUMBER: US/08/591,552
PRIOR APPLICATION NUMBER: US/08/591,552
PRIOR APPLICATION NUMBER: US/08/540,423
PRIOR FILING DATE: 1993-10-22
PRIOR APPLICATION NUMBER: US/08/540,423
PRIOR APPLICATION NUMBER: US/08/540,423
PRIOR APPLICATION NUMBER: US/08/540,632,691
PRIOR APPLICATION NUMBER: US/08/540,632,691
PRIOR APPLICATION NUMBER: US/08/632,691
PRIOR APPLICATION NUMBER: US/08/632,691
PRIOR APPLICATION NUMBER: US/08/632,693
PRIOR FILING DATE: 1996-04-15
PRIOR FILING DATE: 1996-09-19
PRIOR APPLICATION NUMBER: US/08/163,047
PRIOR APPLICATION NUMBER: US/08/163,047
PRIOR APPLICATION NUMBER: US/08/163,047
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                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 73
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SEQ ID NO 7
LENGTH: 71
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Publication No. US20040132659A1
GENERAL INFORMATION:
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                                                                                                                            FILE REFERENCE: UNGR1600
CURRENT APPLICATION NUMBER: US/09/813,484
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/929,847
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                               APPLICANT: Unger, Evan C.
TITLE OF INVENTION: No. 6716412el Method:
TITLE OF INVENTION: Filled Compositions
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PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Agkistrodon piscivorus
ORGANISM: Artificial Sequence
                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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Pred. No. 6e-31;
5; Mismatches
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; OTHER INFORMATION: Completely synthetic sequence US-09-813-484-15
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APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA APPLICANT: Markland, Francis S.
FILE OF INVENTION: CONTORTROSTATIN (CN) AND MET TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR FILING DATE: 1090-06-08
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR APPLICATION NUMBER: US 08/540,603
PRIOR APPLICATION NUMBER: US 08/540,603
PRIOR APPLICATION NUMBER: US 08/745,603
PRIOR FILING DATE: 1996-04-15
PRIOR FILING DATE: 1996-11-08
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Publication No. US20030186884A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 87.7%;
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10712584
Publication No. US20040132659A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CONTORTROSTATIN (CN) /
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1129-338N2/09601388
CURRENT APPLICATION NUMBER: US/10/439,532
CURRENT FILLING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
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TYPE: PRT
ORGANISM: Trimeresurus albolabris
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UNIVERSITY OF SOUTHERN CALIFORNIA
ONTOOTROSTATIN (CN) AND
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Pred. No. 8.6e-31;
4; Mismatches 5
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Pred. No. 8.6e-31;
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RESULT 9 US-10-439-532-8

Sequence 8, Application US/10439532
Publication No. US20030186884A1
GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA TITLE OF INVENTION: CONTORTROSTATIN (CN) AND TITLE OF INVENTION: COTHER CONTIONS FILE REFERENCE: 1279-338NZ/09801388 CURRENT APPLICATION NUMBER: US/10/439,532 CURRENT FILING DATE: 2003-05-16

METHODS FOR ITS USE IN PREVENTING METAS

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; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027Alel Sequency
US-10-046-801-15
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                                                                                                                                     Query Match
Best Local S
Matches 63
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
SEQIT NO 15
LENGTH: 73
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LENGTH: 73
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Best Local
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: US09/460,295
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Charged Lipids and Uses
FILE REFERENCE: UNGRI592
CURRENT APPLICATION NUMBER: US/10/046,801
CURRENT FILING DATE: 2002-05-13
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/540,448
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 08/925,353
PRIOR FILING DATE: 1997-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Trimeresurus albolabris
                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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61 GISAGCPRNPLHA 73
                               61 GISAGCPRNPFHA 73
                                                                                                                                     63;
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                                                                                                    1 EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAGEDCDCGSPANFCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCN
                                                                    EAGEDCDCGSPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCD
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Pred. No. 8.6e-31;
4; Mismatches 5;
                                                                                                                                       Score 386; DB 14;
Pred. No. 2.6e-30;
5; Mismatches 5;
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APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: MAINTAIN, PIANCES S.
APPLICANT: MAINTAIN, PIANCES S.
APPLICANT: MAINTAIN, PIANCES S.
APPLICANT: Riteer, Matthew
ITITE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT APPLICATION NUMBER: US09/591,552
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1993-10-10
PRIOR FILING DATE: 1995-04-15
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-04-15
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-04-15
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-04-15
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-11-08
PRIOR FILING DATE: 1995-11-08
PRIOR FILING DATE: 1995-11-08
PRIOR FILING DATE: 1995-11-08
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RESULT 11
US-10-439-532-2
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; ORGANISM: Trimeresurus gramineus
US-10-439-532-8
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SEQ ID NO 8
LENGTH: 552
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                                                                                                                                                                                                                                                                                  Matches
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Best Local (
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Publication No. US20040132659A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 15
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PRIOR APPLICATION NUMBER: US09/460,295
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Trimeresurus gramineus
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 552
                                                                                                                                                                                    480 EAGEDCDCGSPANPCCDAATCKLIPGAQCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCN 539
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                                                                                           540 GRSAGCPRNPFHA 552
                                                                                                                                61 GISAGCPRNPFHA 73
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Pred. No. 1.5e-29;
7; Mismatches 4;
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Pred. No. 1.5e-29;
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1 EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN

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APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: MARKHAND, FRANCIS S.
APPLICANT: MARKHAND, FRANCIS S.
APPLICANT: Ritter, Matthew
ITILE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS
ITILE OF INVENTION: OTHER CONDITIONS
ITILE OF INVENTION NUMBER: US/10/712,584
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/09/591,552
PRIOR APPLICATION NUMBER: US/09/591,552
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: US/08/540,423
PRIOR FILING DATE: 1996-04-15
PRIOR APPLICATION NUMBER: US/08/632,691
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; ORGANISM: Agkistrodon contortrix
US-10-712-584-2
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US-10-712-584-2
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SEQ ID NO 2
LENGTH: 48
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Publication No. US20030186884A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAS
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-33802/09801398
CURRENT APPLICATION NUMBER: US/10/439,532
CURRENT FILING DATE: 2003-05-16
PRIOR FFLICH DATE: 2003-06-08
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 15
ROPERANCE DESCRIPTION: TOTAL CONTORNEY C
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SEQ ID NO 2
LENGTH: 483
         Matches
                                           Query Match
Best Local Similarity
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Best Local
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PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15
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         Conservative
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Pred. No. 7.4e-28;
5; Mismatches 7;
    5; Mismatches
Score 368; DB 16;
Pred. No. 7.4e-28;
                                                                                                 Length 483;
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Sequence 2, Application US/10078866
Publication No. US20030096393A1
GENERAL INFORMATION:
APPLICANT: FOX, BRIAN A
APPLICANT: FOX, BRIAN A
INFORMATION:
DISINTED OF INVENTION: Disintegrin Homolog, zsnkl6
FILE REFERENCE: 01-05
CURRENT APPLICATION NUMBER: US/10/078,866
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/270,276
PRIOR FILING DATE: 2001-02-20
INUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 478
                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10383588A
PUBLICATION NO. US20040091887A1
GENERAL INFORMATION:
APPLICANT: GUO, Yaw-Wen
APPLICANT: HO, Pei-Hsiun
TITLE OF INVENTION: Mucroslyin and Its Gene
FILE REFERENCE: 87146043-2001
CURRENT APPLICATION NUMBER: US/10/383,588A
CURRENT APPLICATION NUMBER: 2003-07-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
IENCTUP. 462
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US-10-078-866-2
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US-10-383-588A-2
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; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-078-866-2
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Best Local S
Matches 57
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Best Local &
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                                                                                                                                                                                                            FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(463)
                                                                                                                                                                                                                                                                    LENGTH: 463
TYPE: PRT
ORGANISM: Trimeresurus mucrosquamatus
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les 61; Conserv
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                                                    391
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61 GISAGCPRN 69
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                                                     EAGEECDCGSPENPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRCT 450
                                                                           EAGEECDCGAPANPCCDAATCKLRPGAQCAEGLCCDQCRFMKEGTICRMARGDDMDDYCN 60
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                                                                                                                         Score 335; DB 15;
Pred. No. 1.2e-24;
3; Mismatches 9;
                                                                                                                                                             Length 463;
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GENERAL INFORMATION: GUO, YAW-Wen
APPLICANT: GUO, YAW-Wen
APPLICANT: HO, Pei-Hsiun
TITLE OF INVENTION: Mucroslyin and Its Gene
FILE REFERENCE: 87146043-2001
CURRENT APPLICATION NUMBER: US/10/383,588A
CURRENT FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 481
TYPE: PRT
ORGANIGM: Trimeresurus mucrosquamatus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(481)
US-10-383-588A-8
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US-10-383-588A-8
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Search completed: December 3, 2004, 21:49:16 Job time : 105 secs
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                                                                                                                                                                                                                              Query Match 77.4%;
Best Local Similarity 82.6%;
Matches 57; Conservative
                                                                          469
                                                                                                                                                   409 EAGEECDCGSPENPCCDAATCKLRPGAQCAEGLCCDQCRFKKKRTICRRARGDNPDDRCT 468
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                                                                                                        61 GISAGCPRN 69
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                                                                        GOSADCPRN
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Pred. No. 1.2e-24;
3; Mismatches 9;
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Gaps

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